

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: July 3, 2005, 19:37:04 ; Search time 5915 Seconds
(without alignments)
10813.336 Million cell updates/sec

Title: US-09-869-565-1
Perfect score: 1320
Sequence: 1 atggggccgcccggatcgc.....tcattgactggcactagg 1320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hug.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1320	100.0	1320	6	BD270931 PHT recep
2	1264.6	95.8	1335	6	BD266835 PTH funct
3	1243.2	94.2	2051	6	117766 Sequence 3
4	1241.6	94.1	1836	10	RATPTHYR
5	1241.6	94.1	2065	10	RATPTHYR
6	1158.4	87.8	2089	10	BC051981
7	1155.2	87.5	2189	10	BC013446
8	1153.6	87.4	1984	10	MMHPRPR
9	1011.2	76.6	1380	6	BD266846
10	983.8	74.5	1363	6	BD266847
11	977.8	74.1	1380	6	BD266845
12	973.4	73.7	975	6	BD266837
13	966.8	73.2	1948	6	CO867504
14	966.8	73.2	1948	6	AR270690
15	966.8	73.2	1948	6	AX548943
16	966.8	73.2	1948	9	HUMPTHYR
17	965.2	73.1	1947	6	CO714121
18	965.2	73.1	2010	6	117767
19	965.2	73.1	2095	9	HSPHR

20 965.2 73.1 2171 9 HSU17418
21 961.2 72.8 1785 6 CO831233
22 959.6 72.7 1782 6 AX280939
23 959.6 72.7 1782 9 AY449732
24 933.8 70.7 1770 4 AF288463
25 930 70.5 1002 6 BD266836
26 902.2 68.3 2177 4 AF167095
27 893 67.7 2067 4 SSU18315
28 892.2 67.6 1859 4 AY328401
29 693.2 52.5 1878 4 OPOPTHYR
30 691.6 52.4 1863 6 117765
31 681.2 51.6 1862 6 117764
32 554.6 42.0 1609 6 BD249740
33 554.6 42.0 1609 6 AR302320
34 554.6 42.0 2129 5 AF132084
35 532.6 40.3 2928 6 CO831243
36 462.4 35.0 637 6 AX421448
37 415.4 31.5 2429 5 AF132082
38 393.4 29.8 1219 10 AB012944
39 393.4 29.8 231335 2 AC098311
40 393.4 29.8 238330 2 AC114361
41 391.4 29.7 515 10 RATPTHYR
42 390.6 29.6 2152 5 AF132085
43 387.4 29.3 1653 9 AY497546
44 387.4 29.3 2003 6 AR182589
45 387.4 29.3 2152 6 BD249741

ALIGNMENTS

RESULT 1
BD270931
LOCUS BD270931 1320 bp DNA linear PAT 17-JUL-2003
DEFINITION PHT receptor and screening assay utilizing the same.
ACCESSION BD270931
VERSION BD270931.1 GI:33080699
KEYWORDS JP 2002534081-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1320)
AUTHORS Gardella, J., Kronenberg, H.M. and Jr, J.T.P.
TITLE PHT receptor and screening assay utilizing the same.
JOURNAL Patent: JP 2002534081-A 1 15-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002534081-A/1
PD 15-OCT-2002
PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS JR PC
CL2N15/09, C07K14/72, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC CL2P21/02, C12Q1/02, C12N15/00, C12N5/00
CC Description of Artificial Sequence: cDNA
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
(1)..(1308).

FEATURES

source
1..1320
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 1320; DB 6; Length 1320;
Best Local Similarity 100.0%; Pred. No. 3.4e-265;
Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGGCCGCCCGGATCGCACCAGCTGCTCTCTCTGCTGCCAGTCTCAGC 60
DB 1 ATGGGGCCGCCCGGATCGCACCAGCTGCTCTCTCTGCTGCCAGTCTCAGC 60
QY 61 TCCGCATATGCGTGGAGGTATTGTACCGCTAGCATGATGTACACCGTGGGATCTCC 120

Db 1141 GCCAAGCAGGGGCTCCAGCCACTGAGACTGAAACCTACAGTCACTATGGCGTTCCC 1200
Qy 1201 AAGGACGATGGATTCCTTAACGGCTCCTGCTCAGGCTCGATGAGGAGGCTCCGGGTCT 1260
Db 1201 AAGGACGATGGATTCCTTAACGGCTCCTGCTCAGGCTCGATGAGGAGGCTCCGGGTCT 1260
Qy 1261 GCAGCGCCGCTCCATTTGTCAGGAGGATGGGAAACAGTCACTGTCAGTGGGCACTAGG 1320
Db 1261 GCAGCGCCGCTCCATTTGTCAGGAGGATGGGAAACAGTCACTGTCAGTGGGCACTAGG 1320

RESULT 2
BD266835
LOCUS 1335 bp DNA linear PAT 17-JUL-2003
DEFINITION PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules.
ACCESSION BD266835
VERSION BD266835.1 GI:33076603
KEYWORDS JP 2002533115-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1335)
AUTHORS Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
TITLE PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules
JOURNAL Patent: JP 2002533115-A 4 08-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002533115-A/4
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591171
PR 31-DEC-1998 US 60/114577
PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI
JUEPPNER
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
A61P19/10,
PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: modified PTH receptor CC
sequence
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
1..1335
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source

ORIGIN

Query Match 95.8%; Score 1264.6; DB 6; Length 1335;
Best local Similarity 97.7%; Pred. No. 1.3e-253;
Matches 1304; Conservative 0; Mismatches 4; Indels 27; Gaps 1;

Qy 1 ATGGGGCGCCCGGATCGCACCCAGCTGGCGCTCTCTCTCTGCTGCCAGTGTCTCAGC 60
Db 1 ATGGGGCGCCCGGATCGCACCCAGCTGGCGCTCTCTCTCTGCTGCCAGTGTCTCAGC 60
Qy 61 TCCGCATATCGCTG-----GAGGTATTTGACCGCTA 93
Db 61 TCCGCCTATCGCGCGCAACACGACGACGCGGAGGCGAGGTATTTGACCGCTA 120
Qy 94 GGCATGATCTACACCGTGGGATCTCCATGCTCTCGCTCCCTCCCTCAGGTGGCTGTCTC 153
Db 121 GGCATGATCTACACCGTGGGATCTCCATGCTCTCGCTCCCTCCCTCAGGTGGCTGTCTC 180
Qy 154 ATCTGTGCTCTATTTTAGCGGCTGCACTGCACGCGCAACTACATCCACATGCAATGTC 213
Db 181 ATCTGTGCTCTATTTTAGCGGCTGCACTGCACGCGCAACTACATCCACATGCAATGTC 240
Qy 214 CTGTGCTTTATGCTGCGCGCGGAGCATCTTGTGAAGGACGCTGTGCTCTACTCTGGC 273

Db 1141 GCCAAGCAGGGGCTCCAGCCACTGAGACTGAAACCTACAGTCACTATGGCGTTCCC 1200
Qy 1201 AAGGACGATGGATTCCTTAACGGCTCCTGCTCAGGCTCGATGAGGAGGCTCCGGGTCT 1260
Db 1201 AAGGACGATGGATTCCTTAACGGCTCCTGCTCAGGCTCGATGAGGAGGCTCCGGGTCT 1260
Qy 1261 GCAGCGCCGCTCCATTTGTCAGGAGGATGGGAAACAGTCACTGTCAGTGGGCACTAGG 1320
Db 1261 GCAGCGCCGCTCCATTTGTCAGGAGGATGGGAAACAGTCACTGTCAGTGGGCACTAGG 1320

RESULT 2
BD266835
LOCUS 1335 bp DNA linear PAT 17-JUL-2003
DEFINITION PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules.
ACCESSION BD266835
VERSION BD266835.1 GI:33076603
KEYWORDS JP 2002533115-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1335)
AUTHORS Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
TITLE PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules
JOURNAL Patent: JP 2002533115-A 4 08-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002533115-A/4
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591171
PR 31-DEC-1998 US 60/114577
PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI
JUEPPNER
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
A61P19/10,
PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: modified PTH receptor CC
sequence
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
1..1335
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source

ORIGIN

Query Match 95.8%; Score 1264.6; DB 6; Length 1335;
Best local Similarity 97.7%; Pred. No. 1.3e-253;
Matches 1304; Conservative 0; Mismatches 4; Indels 27; Gaps 1;

Qy 1 ATGGGGCGCCCGGATCGCACCCAGCTGGCGCTCTCTCTCTGCTGCCAGTGTCTCAGC 60
Db 1 ATGGGGCGCCCGGATCGCACCCAGCTGGCGCTCTCTCTCTGCTGCCAGTGTCTCAGC 60
Qy 61 TCCGCATATCGCTG-----GAGGTATTTGACCGCTA 93
Db 61 TCCGCCTATCGCGCGCAACACGACGACGCGGAGGCGAGGTATTTGACCGCTA 120
Qy 94 GGCATGATCTACACCGTGGGATCTCCATGCTCTCGCTCCCTCCCTCAGGTGGCTGTCTC 153
Db 121 GGCATGATCTACACCGTGGGATCTCCATGCTCTCGCTCCCTCCCTCAGGTGGCTGTCTC 180
Qy 154 ATCTGTGCTCTATTTTAGCGGCTGCACTGCACGCGCAACTACATCCACATGCAATGTC 213
Db 181 ATCTGTGCTCTATTTTAGCGGCTGCACTGCACGCGCAACTACATCCACATGCAATGTC 240
Qy 214 CTGTGCTTTATGCTGCGCGCGGAGCATCTTGTGAAGGACGCTGTGCTCTACTCTGGC 273

241	Db	CTGTCGTTTATGCTGCGCGCGAGGACATCTTCTGTGAAGACGCTGTGCTCTACTCTGGC	300
274	Qy	TTCA CGCTGGATGAGCGCGAGCGCCTCACAGAGGAAGATTGCA CATCATCGCGCAGGTG	333
301	Db	TTCA CGCTGGATGAGCGCGAGCGCCTCACAGAGGAAGATTGCA CATCATCGCGCAGGTG	360
334	Qy	CCACCTCGCGCGCGCTGCGCGCGTAGGCTACGCTGGCTGCGCGGTGGCGGTGACCTTC	393
361	Db	CCACCTCGCGCGCGCTGCGCGCGTAGGCTACGCTGGCTGCGCGGTGGCGGTGACCTTC	420
394	Qy	TTCTCTTACTTTCCTGGCTTACCAACTACTTACTGGATCTGTGGTGGAGGGCTGTACTTGCAC	453
421	Db	TTCTCTTACTTTCCTGGCTTACCAACTACTTACTGGATCTGTGGTGGAGGGCTGTACTTGCAC	480
454	Qy	AGCCTCATCTTTCATGGCCTTTTCTCAGAGAAGTAAGTACCTGTGGGCTTTCA CCAATCTTT	513
481	Db	AGCCTCATCTTTCATGGCCTTTTCTCAGAGAAGTAAGTACCTGTGGGCTTTCA CCAATCTTT	540
514	Qy	GGCTGGGGTCTACCGGCTGTCTTGGTGGCTGTGTGGGTGGGTGGGTGTCAGAGCAACTTGGCC	573
541	Db	GGCTGGGGTCTACCGGCTGTCTTGGTGGCTGTGTGGGTGGGTGGGTGTCAGAGCAACTTGGCC	600
574	Qy	AACACTGGGTGCTGGGATCTGAGCTCTCGGGCACAGAAGTGGATCATTCAGGTGCCCATC	633
601	Db	AACACTGGGTGCTGGGATCTGAGCTCTCGGGCACAGAAGTGGATCATTCAGGTGCCCATC	660
634	Qy	CTGGCATCTGTGTGCTCAACTTCATCCTTTTTTATCAACATCATCCGGGTGCTTTGCCACT	693
661	Db	CTGGCATCTGTGTGCTCAACTTCATCCTTTTTTATCAACATCATCCGGGTGCTTTGCCACT	720
694	Qy	AAGCTTCGGGAGACCAATGCGGGCGGTGTGACACGAGGACGAGTACCGGAAGCTGCTC	753
721	Db	AAGCTTCGGGAGACCAATGCGGGCGGTGTGACACGAGGACGAGTACCGGAAGCTGCTC	780
754	Qy	AGGTCCACGTTGGTGTCTGTCGCCCTCTTTGGTGTGCACTACACCGTCTTATGGCCCTTG	813
781	Db	AGGTCCACGTTGGTGTCTGTCGCCCTCTTTGGTGTGCACTACACCGTCTTATGGCCCTTG	840
814	Qy	CCGTACACCGAGGTCTCAGGGACATTTGGCAGATCCAGATGCATTTATGAGATGCTCTTC	873
841	Db	CCGTACACCGAGGTCTCAGGGACATTTGGCAGATCCAGATGCATTTATGAGATGCTCTTC	900
874	Qy	AATCTCTTCCAGGATTTTTTTGGTGGCATCATATACCTGTCTTTCGAATGTTGAGGTGCAG	933
901	Db	AATCTCTTCCAGGATTTTTTTGGTGGCATCATATACCTGTCTTTCGAATGTTGAGGTGCAG	960
934	Qy	GCAGAGATTAGGAAGTATGAGCGCGCTGGACATCGGCGTTGGACTTCAGCGCAAGCA	993
961	Db	GCAGAGATTAGGAAGTATGAGCGCGCTGGACATCGGCGTTGGACTTCAGCGCAAGCA	1020
994	Qy	CGAAGTGGGATGACAGCTACAGCTATGGCCCAATGGTGTCTCACAGAGTGTGACCAAT	1053
1021	Db	CGAAGTGGGATGACAGCTACAGCTATGGCCCAATGGTGTCTCACAGAGTGTGACCAAT	1080
1054	Qy	GTGGGCCCCGTGCAGACTCAGCCTCCCTCTAGCCCCCGCTGCTCTCTGCCACTTACC	1113
1081	Db	GTGGGCCCCGTGCAGACTCAGCCTCCCTCTAGCCCCCGCTGCTCTCTGCCACTTACC	1140
1114	Qy	AATGGCCACTCCAGCTGCTGGCCCATGCCCAGCCAGGGGCTCAGGCCACTGAGACTGAA	1173
1141	Db	AATGGCCACTCCAGCTGCTGGCCCATGCCCAGCCAGGGGCTCAGGCCACTGAGACTGAA	1200
1174	Qy	ACCTTACAGTCACTATGGCGGTTTCCCAAGGACGATGGATTCTTTAAGCGTCTCTGTCTCA	1233
1201	Db	ACCTTACAGTCACTATGGCGGTTTCCCAAGGACGATGGATTCTTTAAGCGTCTCTGTCTCA	1260
1234	Qy	GGCTTGGATGAGGAGGCTCTCGGGTCTGCGCGCGCCTCCATTTGTTGCAGGAAGTGG	1293
1261	Db	GGCTTGGATGAGGAGGCTCTCGGGTCTGCGCGCGCCTCCATTTGTTGCAGGAAGTGG	1320
1294	Qy	GAACAGTCACTGTGA	1308
1321	Db	GAACAGTCACTGTGA	1335

```
Qy 733 CAGCAGTACCGAGCTGCTCAGGTCACAGTGGTGTCTCGTCCGCTCTTTGGTGTGCAC 792
Db |||||
Qy 1273 CAGCAGTACCGAAGCTGCTCAGGTCACAGTGGTGTCTCGTCCGCTCTTTGGTGTCCAC 1332
Db |||||
Qy 793 TACACCGTCTTCATGGCTTGGCCGTACACCGAGGTCCTCAGGGAATTTGTGCGAGATCCAG 852
Db |||||
Qy 1333 TACACCGTCTTCATGGCTTGGCCGTACACCGAGGTCCTCAGGGAATTTGTGCGAGATCCAG 1392
Db |||||
Qy 853 ATGATTTATGAGTGTCTTCAACTCTTCACGGATTTTGTGTCATATATCTGT 912
Db |||||
Qy 1393 ATGATTTATGAGTGTCTTCAACTCTTCACGGATTTTGTGTCATATATCTGT 1452
Db |||||
Qy 913 TTCTGCAATGCTGAGGTGCGAGGAGATTTAGGAAGTCATGGAGCCGCTGGACACTGGCG 972
Db |||||
Qy 1453 TTCTGCAATGCTGAGGTGCGAGGAGATTTAGGAAGTCATGGAGCCGCTGGACACTGGCG 1512
Db |||||
Qy 973 TTGGACTTCAAGCCCAAGACCAAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1032
Db |||||
Qy 1513 TTGGACTTCAAGCCCAAGACCAAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1572
Db |||||
Qy 1033 TCTCACAGAGTGTGACCAATGTGGGCCCGCTGCAGGATCTCAGCCTCCCGCTCAGCCCC 1092
Db |||||
Qy 1573 TCTCACAGAGTGTGACCAATGTGGGCCCGCTGCAGGATCTCAGCCTCCCGCTCAGCCCC 1632
Db |||||
Qy 1093 CGCCTGCTCTGCTCACTACCAATGGCCACTCCAGCTGCTGGCCATGCCAGCCAGGG 1152
Db |||||
Qy 1633 CGCCTGCTCTGCTCACTACCAATGGCCACTCCAGCTGCTGGCCATGCCAGCCAGGG 1692
Db |||||
Qy 1153 GCTCAGCACTGAGACTGAAACCTTACCAGTCACTATGGCGTTCCTCAAGGACGATGGA 1212
Db |||||
Qy 1693 GCTCAGCACTGAGACTGAAACCTTACCAGTCACTATGGCGTTCCTCAAGGACGATGGA 1752
Db |||||
Qy 1213 TTCCTTAACGGCTCTGCTCAGGCTGAGGAGGAGGCTCCGGGTCTGGCGGCGCCCT 1272
Db |||||
Qy 1753 TTCCTTAACGGCTCTGCTCAGGCTGAGGAGGAGGCTCCGGGTCTGGCGGCGCCCT 1812
Db |||||
Qy 1273 CCATTGTTGAGGAGGAGTGGGAACAGTATGATGCTGGGCACTAGG 1320
Db |||||
Qy 1813 CCATTGTTGAGGAGGAGTGGGAACAGTATGATGCTGGGCACTAGG 1860
Db |||||
```

```
RESULT 4
RATPTRH RATPTRH 1836 bp mRNA linear ROD 08-JUN-1995
LOCUS Rat parathyroid hormone/parathyroid hormone related-peptide
DEFINITION receptor mRNA, complete cds.
ACCESSION L19475
VERSION L19475.1 GI:467316
KEYWORDS parathyroid hormone; parathyroid hormone receptor; parathyroid hormone-related protein; parathyroid hormone-related receptor.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1836)
AUTHORS Pausova,Z., Bourdon,J., Clayton,D., Mattei,M.G., Seldin,M.F., Janic,N., Riviere,M., Szpirer,J., Levan,G., Szpirer,C., Goltzman,D. and Hendy,G.N.
TITLE Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line: chromosomal assignment of the gene in the human, mouse, and rat genomes
JOURNAL Genomics 20 (1), 20-26 (1994)
MEDLINE 94292182
PUBMED 8020952
COMMENT Original source text: Rattus norvegicus cDNA to mRNA.
FEATURES
source
Location/Qualifiers
1..1836
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/cell_line="UMR 106"
```

```

/cell_type="osteosarcoma"
46..1821
/codon_start=1
/product="parathyroid hormone/parathyroid hormone related-peptide receptor"
/protein_id="AAA68098.1"
/db_xref="GI:467317"
/translation="MGAARIAPSLALLCCPVLSSAYALVADDDVFTKEQIIFLLHRA
QAQCDLLKEVLTAAANTIMESDKWTTPASTSGKPRKASGKFPYPSKKNQDVPTGSR
RGRPCPLNDNIVCWPLGAGEVAVAPCPDIYIDFNHGHAYRCDNRGSMVWVPGH
NRTWNYSLCLFMTNRETREREVDFRLGMIYTVGYSMSLASLTVALIILAYPRRLCT
RNYIHMFVLSFMLRAASI FVKDVAIVLYSGFTLDEARLTTEELHIIAQVPPPPAAAV
GVAGCRVATFEFLIATNYVLLVEGLVLSLIFMAFFSEKKYLGFTIFGMLPAV
FVAVWVGRATLANTGCDLSSGHKKWIIQVPLIASVLFNFILFINIIVLATPKRET
NAGCDTRQYRKLLRSTLIVLPFGVHTIVFMALPYTEVSGTLMOIQHMYMLFNSF
QQPFAIITYFCNVEQVABIRKRSWSWTIALDFKRRKRSQSSSYSGPMSVTSVNV
GPRAGLSPLSPRLPPATTNGHSQLFHGAKPGAPATETETLPTVMAVPKDDGFLNSC
SGLDERASGSARPPPLLBQEWETVM"
46..117
sig_peptide
mat_peptide
118..1818
/product="parathyroid hormone/parathyroid hormone related-peptide receptor"
ORIGIN
Query Match 94.1%; Score 1241.6; DB 10; Length 1836;
Best Local Similarity 99.7%; Pred. No. 7.8e-249; Indels 0; Gaps 0;
Matches 1244; Conservative 0; Mismatches 4;
Qy 73 CTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATPACTCCATGTCTCTCGCC 132
Db |||||
Qy 586 CGGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATPACTCTCTCGCC 645
Db |||||
Qy 133 TCCTCAGCGTGTCTGTCTATCTCTGGGCTATTTTAGCGGGCTGACTGCACGCGCAAC 192
Db |||||
Qy 646 TCCTCAGCGTGTCTGTCTATCTCTGGGCTATTTTAGCGGGCTGACTGCACGCGCAAC 705
Db |||||
Qy 193 TACATCCACATGACACATGTTTCTGTGCTTTATGCTCGCGCCGCGAGCATCTTCGTGAAG 252
Db |||||
Qy 706 TACATCCACATGACACATGTTTCTGTGCTTTATGCTGCGCCGCGAGCATCTTCGTGAAG 765
Db |||||
Qy 253 GACGCTGTGCTTACTCTGCTTACGCTGGATGAGGCCGAGCGCCTCAGAGGGAAGAG 312
Db |||||
Qy 766 GACGCTGTGCTTACTCTGCTTACGCTGGATGAGGCCGAGCGCCTCAGAGGGAAGAG 825
Db |||||
Qy 313 TTGCACATCATCGCGAGGTGCGACCTCGCGCGCGCGCTGCGCGGTAGGCTAGCTGGC 372
Db |||||
Qy 826 TTGCACATCATCGCGAGGTGCGACCTCGCGCGCGCGCTGCGCGGTAGGCTAGCTGGC 885
Db |||||
Qy 373 TGCGCGGTGGCGGTGACCTTCTTCTTCTACTTCTGCTACCACTACTACTGATCCTG 432
Db |||||
Qy 886 TGCGCGGTGGCGGTGACCTTCTTCTTCTACTTCTGCTACCACTACTACTGATCCTG 945
Db |||||
Qy 433 GTGGAGGGGCTGTACTTGCACAGCCTCATCTTCATGCGCCTTTTCTCAGAGAGAAGTAC 492
Db |||||
Qy 946 GTGGAGGGGCTGTACTTGCACAGCCTCATCTTCATGCGCCTTTTCTCAGAGAGAAGTAC 1005
Db |||||
Qy 493 CTGTGGGGCTTACCATCTTTTGGCTGGGTCTACCGGTGTCTCTGTTGGGTGTGTGGGT 552
Db |||||
Qy 1006 CTGTGGGGCTTACCATCTTTTGGCTGGGTCTACCGGTGTCTCTGTTGGGTGTGTGGGT 1065
Db |||||
Qy 553 GGTGTGAGAGCAACCTTTGGCCAAACACTGGGTGTGGGATCTGAGCTCCGCGGCAAGAAG 612
Db |||||
Qy 1066 GGTGTGAGAGCAACCTTTGGCCAAACACTGGGTGTGGGATCTGAGCTCCGCGGCAAGAAG 1125
Db |||||
Qy 613 TGGATCATCCAGGTGCCCCATCTCTGGGATCTGTTGTGTCTCACTTCACTCTTTTATCAAC 672
Db |||||
Qy 1126 TGGATCATCCAGGTGCCCCATCTCTGGGATCTGTTGTGTCTCACTTCACTCTTTTATCAAC 1185
Db |||||
Qy 673 ATCATCCGGGTGCTTGGCACTAAGCTTCGGAGACCAATGCGGGCGGTGTGACCCAGG 732
Db |||||
Qy 1186 ATCATCCGGGTGCTTGGCACTAAGCTTCGGAGACCAATGCGGGCGGTGTGACCCAGG 1245
Db |||||
Qy 733 CAGCAGTACCGAAGTGTCTCAGGTCCACGCTTGGTGTCTGTCGCGGCTCTTTTGGTGTGCAC 792
Db |||||
```


Db	722	CGGAGGTA	TTTGACCGCGCTGGGCA	TGATCTACACCGTGGGATATTCATGTC	CTCTTTGCC	781	
Qy	133	TCCCTCA	CGGTGTGTCTGCTCA	TCCTGGCCCTATTTTAGCGCGCTGCA	CTGCACGCGCAAC	192	
Db	782	TCCCTCAC	CGGTGTGTGCTCAT	CTTAGCCTATTTTAGCGCGCTGCA	CTGCACGCGCAAC	841	
Qy	193	TAGATCCAC	ATGACATGTTTCCTGTCTGTTAT	TGCTGCGCGCGCGAGCATCTTCGTGAAG	252		
Db	842	TACATCCAC	ATGACATGTTTCCTGTCTGTTAT	TGCTGCGCGCGCGAGCATCTTCGTGAAG	901		
Qy	253	GACGCTGT	GCTTACTCTGGGCTTCAC	CGCTGGATGAGCGCGAGCCCTCACAGAGGAAGAG	312		
Db	902	GACGCTGT	GCTTACTCTGGGCTTCAC	CGCTGGATGAGCGCGAGCCCTCACAGAGGAAGAG	961		
Qy	313	TTGCACAT	CAATCGCGAGGTGCCAC	TCCCGCGCGCTCGCGCTAGGCTACGCTGGC	372		
Db	962	TTGCATAT	CAATCGCGAGGTGCCAC	TCCCGCGCGCTCGCGCTAGGCTACGCTGGC	1021		
Qy	373	TGCGCGT	TGGCGGTGACCTTCTCTACT	CTTCTGTGCTTACCACTACTACTTGGATCCTG	432		
Db	1022	TGCGGTGT	TGGCGGTGACCTTCTCTACT	CTTCTGTGCTTACCACTACTACTTGGATCCTG	1081		
Qy	433	GTGAGGCG	GTACTTGTGCA	CAGCCTCATCTTCA	TGSCCTTTTCTCAGAGAGAAGTAC	492	
Db	1082	GTGAGGCG	GTACTTGTGCA	CAGCCTCATCTTCA	TGSCCTTTTCTCAGAGAGAAGTAT	1141	
Qy	493	CTGTGGG	CGCTTCA	CCATCTTTGGCTGGGGTCTAC	CGGCTGTCTTTCGTGGGCTGTGTGGGTC	552	
Db	1142	CTGTGGG	CGCTTCA	CCATCTTTGGCTGGGGTCTAC	CGGCTGTCTTTCGTGGGCTGTGTGGGTC	1201	
Qy	553	GGTGTCA	GAGCAACTTTGGGCA	CACTGGGTGTGGGATCTG	AGCTCCGGGCA	CAGAAG	612
Db	1202	GGTGTCA	GAGCAACTTTGGGCA	CACTGGGTGTGGGATCTG	AGCTCCGGGCA	CAGAAG	1261
Qy	613	TGGATCAT	CAGGTGCCATCTGGCAT	CTGTGTGCTCAACTTCATCTTTTATCAAC	672		
Db	1262	TGGATCAT	CAGGTGCCATCTGGCAT	CTGTGTGCTCAACTTCATCTTTTATCAAC	1321		
Qy	673	ATCATCC	GGGTGCTTGC	CACTTAAGCTTTGGGAGACCAAT	CGGCGCGGTGTGACAC	CAGG	732
Db	1322	ATCATCC	GGGTGCTTGC	CACTTAAGCTTTGGGAGACCAAT	CGGCGCGGTGTGACAC	CAGG	1381
Qy	733	CAGCAGT	ACCGGAAGCTGT	CAAGTCCAGTGTGTGCTGTGTCGCGCTCTTTTGTGTGCAC	792		
Db	1382	CAGCAGT	ACCGGAAGCTGT	CAAGTCCAGTGTGTGCTGTGTCGCGCTCTTTTGTGTGCAC	1441		
Qy	793	TACACCG	CTCTCATGGCTTGGCGT	CAACCGAGTCTCAGGGACATTTGTGGCAGATCCAG	852		
Db	1442	TACACCG	CTCTCATGGCTTGGCGT	CAACCGAGTCTCAGGGACATTTGTGGCAGATCCAG	1501		
Qy	853	ATGCATTA	TGAGATGCTCTTCA	ACTCCCTCCAGGGAATTTTGTGGCATCATATACTGT	912		
Db	1502	ATGCATTA	TGAGATGCTCTTCA	ACTCCCTCCAGGGAATTTTGTGGCATCATATACTGT	1561		
Qy	913	TTCTGCA	ATGGTGTGACGGCAGAGAT	TAGGAAGTCA	TGGAGCCGCTGGACACATGGCG	972	
Db	1562	TTCTGCA	ATGGTGTGACGGCAGAGAT	TAGGAAGTCA	TGGAGCCGCTGGACACATGGCA	1621	
Qy	973	TTGGACTT	CAAGCGCAAGCAG	AGTGGAGTAGCAGCTAC	AGCTATGGCCCAATGGTG	1032	
Db	1622	TTGGACTT	CAAGCGTAAAGCA	CGAAGTGGGAGTAGCAGCTAC	AGCTATGGCCCAATGGTG	1681	
Qy	1033	TCTCAC	ACGAGTGTGACAA	TGTGGGCGCGGTG	CAGAGCTCAGCCTCCCGCTCAGCCCC	1092	
Db	1682	TCACAC	ACGAGTGTGACAA	TGTGGGCGCGGTG	CAGAGCTTCCCGCTTACGCCCC	1741	
Qy	1093	CGCCTG	CTCTG	CACTACCAATGGGCAC	TCCAGCTGCTGGCCATG	CGCAAGCCAGGG	1152
Db	1742	CGCCTG	CTCTG	CACTACCAATGGGCAC	TCCAGCTGCTGGCCATG	CGCAAGCCAGG	1801
Qy.	1153	GCTCC	AGC	CACTAGTAAACCTTAC	AGTCACTATGGCGGTTCC	CAAGAGCAGATGGA	1212
Db	1802	GCTCC	AGC	CACTAGTAAACCTTAC	AGTCACTATGGCGGTTCC	CAAGAGCAGC	1861

Qy	1213	TTCTTAACGGCTCTCTGCTCAGCGCTTGATGAGAGGCTCTCGGGTCTCGCGCGCGCCCT 12172
Db	1862	TTCTTAATGGCTCTCTGCTCGGCTCTGGATGAGAGGCTCTCTGGTCTCGCGCGCCACCT 1921
Qy	1273	CCATTCTTGAGGAAGATGCGGAACAGTCATGTGACTGGGCACTAGG 1320
Db	1922	CCATTGTGTCAGGAAGAATGCGGAACAGTCATGTGACTGGGCACTAAG 1969
RESULT 7		
BC013446		
LOCUS	BC013446	2189 bp mRNA linear ROD 29-JUN-2004
DEFINITION	Mus musculus parathyroid hormone receptor 1, mRNA (cDNA clone	
	MGC:18447 IMAGE:4241234), complete cds.	
ACCESSION	BC013446	
VERSION	BC013446.1	GI:15488603
KEYWORDS	MGC.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 2189)	
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zerborg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2189)	
AUTHORS	Strausberg,R.	
TITLE	Direct Submission	
JOURNAL	Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk Email: cgapsb-rc@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcdpaxil@stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 25 Row: d Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755221.	
source	Location/Qualifiers 1. .2189 /organism="Mus musculus"	

```
/mol_type="mRNA"  
/strain="FVB/N"  
/db_xref="taxon:10090"  
/clone="MGC:18447 IMAGE:4241234"  
/tissue_type="Kidney, normal, 5 month old male mouse."  
/clone_lib="NCI CGAP_Kid14"  
/lab_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
1. 2189  
/gene="Pthr1"  
/genes="Pthr1"  
/note="synonyms: Pthr, PPR, PTHrP"  
/db_xref="LocusID:19228"  
/db_xref="MGI:97801"  
257..2032  
/gene="Pthr1"  
/codon_start=1  
/product="parathyroid hormone receptor 1"  
/protein_id="AAH13446.1"  
/db_xref="GI:15488604"  
/db_xref="LocusID:19228"  
/db_xref="MGI:97801"  
/translation="MGTAIAPSLALLCCPVLSAYALVADVDTKBEQIFLLHRA  
QAQDKLLKLEHTANIMESDKGTPASTSGPRKEKAPGKFPYPSKKNKOVPTGSR  
RRGRPCLPEDNIVCPPLGAPGVDPDIYDFNKHGHAYRCDRNGSWEVFGH  
RNTWANYSECLKMTRETEREVDFRLGMIYTVGYSMLASLTAVAILLAYFRLHCT  
RNYLHMEPLFSWLRASIFVKDAVLSGFTLDEASRLTEELHIIAOPVPPAAAV  
GYAGCRVATFFLYFLATNYWIIWEGLYLHSLIPWAFSEKKYLGFTIPGHLPAV  
FVAVGVGRTALANTGWDLSUSSHKKWIIQVPIASVNLFIILINIRIATLKRET  
NAGRCPTQRYKLLSLTLVPLFGVHYTFVMAIPYEVSGTLMQIQMHYEMLFNSF  
QGFFVAILYFCNCEVQAEIRKSWRMTALDFRKARSGSSSYSGYPMVSHTSVTNV  
GPRAGLSLPLSLPATNTHSOLPGHAKPGAPATENETIPVTMTVPKDDGLNGSC  
SGLDEASGSRPPLQLQBEWEIVM"
```

ORIGIN

Query Match 87.5%; Score 1155.2; DB 10; Length 2189;

Best Local Similarity 95.4%; Pred. No. 8.4e-231;

Matches 1190; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY	73	CTGGAGGATTTGACCGCGTAGGATGATCTACACCGTGGGATCTCCATGCTCTCGCC	132
DB	797	CGGGAGGATAATTGACCGCGTAGGATGATCTACACCGTGGGATTTCCATGCTCTCGCC	856
QY	133	TCCCTCAGCGTGGTGTGCTCATCTCGCGCTATTTTAGCGGCTGCACTGACGCGCAAC	192
DB	857	TCCCTCAGCGTGGTGTGCTCATCTAGCGCTATTTTAGCGGCTGCACTGACGCGCAAC	916
QY	193	TACATCACATGACATGTTCTCTGTTATGCTGCGCGCGGAGCATCTTCTGTAAG	252
DB	917	TACATCACATGACATGTTCTCTGTTATGCTGCGCGCGGAGCATCTTCTGTAAG	976
QY	253	GACGCTGTCTACTCTGGCTTACCGTGGAGGCGCGGAGCGGCTCACAGAGGAAG	312
DB	977	GACGCTGTCTACTCTGGCTTACCGTGGAGGCGCGGAGCGGCTCACAGAGGAAG	1036
QY	313	TTGCACATCATCGCGGAGGTGCCACCTCCGCGCGCGCTGCGCGGTAGGCTACGCTGGC	372
DB	1037	TTGCATATCATCGCGGAGGTGCCACCTCCACCGCGCGCTGCGCGGTAGGCTGGC	1096
QY	373	TGCGCGGTGGCGGTGACCTTCTCTACTTCTGCTGCTACCACTACTGATCTG	432
DB	1097	TGCGCGGTGGCGGTGACCTTCTCTACTTCTGCTGCTACCACTACTGATCTG	1156
QY	433	GTGGAGGGCTGTACTTGCACAGCGCTCATCTTCAATGCGCTTTTCTCAGAGAGACTAC	492
DB	1157	GTGGAGGGCTGTACTTGCACAGCGCTCATCTTCAATGCGCTTTTCTCAGAGAGAGTAT	1216
QY	493	CTGTGGGCTTCCACATCTTTGGCTGGGGTCTACCGGCTGTCTTCTGGCTGTGTGGGTC	552
DB	1217	CTGTGGGCTTCCACATCTTTGGCTGGGGTCTCCCGGCTGTCTTCTGGCTGTGTGGGTC	1276
QY	553	GGTGTACAGACAACTTTGGCCAAACACTGGGTGTGGGATCTGAGCTCGGGGCAACAAG	612
DB	1277	GGTGTACAGACAACTTTGGCCAAACACTGGGTGTGGGATCTGAGCTCTGGGCAACAAG	1336

QY	613	TGGATCATCCAGTGGCCATCTGTGCTCAACTTCACTCTCTTTTATCAAC	672
DB	1337	TGGATCATCCAGTGGCCATCTGTGCTCAACTTCACTCTCTTTTATCAAC	1396
QY	673	ATCATCCGGGTGCTTCCCACTAAGCTTCGGGAGACCAATTCGGGCGGTGTGACACAGG	732
DB	1397	ATCATCCGGGTGCTTCCCACTAAGCTTCGGGAGACCAATTCGGGCGGTGTGACACAGG	1456
QY	733	CAGCAGTACGGGAAGCTGCTCAGGTCACAGTTCGCTGCTGCTGCTCTTTGGTGGCAC	792
DB	1457	CAGCAGTACGGGAAGCTGCTCAGGTCACAGTTCGCTGCTGCTGCTCTTTGGTGGCAC	1516
QY	793	TACACCGTCTTTCATGCGCTTTCGCTACACCGAGGCTCTCAGGACACTTGTGGCAGATCCAG	852
DB	1517	TACACCGTCTTTCATGCGCTTTCGCTACACCGAGGCTCTCAGGACACTTGTGGCAGATCCAG	1576
QY	853	ATGCATTATGAGATGCTCTTCAACTCTTCCAGGAGATTTTGTGTCCTATCATATCTGT	912
DB	1577	ATGCATTATGAGATGCTCTTCAACTCTTCCAGGAGATTTTGTGTCCTATCATATCTGT	1636
QY	913	TTCTGCAATGCTGAGTGCAGGACAGATTTAGGAAGTCTTTGGAGCGCTGGACACTGGCG	972
DB	1637	TTCTGCAATGCTGAGTGCAGGACAGATTTAGGAAGTCTTTGGAGCGCTGGACACTGGCA	1696
QY	973	TTGGACTTCAAGCGCAAGCAGCAAGTGGAGTAGCAGCTTACAGCTATGCCCCAATGGTG	1032
DB	1697	TTGGACTTCAAGCGTAAAGCAAGTGGAGTAGCAGCTTACAGCTATGCCCCAATGGTG	1756
QY	1033	TCTCACACAGTGTGACCAATGTTGGGCGCGCTGAGGACTCAGCTCTCCCTCCTCAGCCCC	1092
DB	1757	TCACACACAGTGTGACCAATGTTGGGCGCGCTGAGGACTCAGCTCTCCCTCCTCAGCTCC	1816
QY	1093	CGCTGCTCTCTGCTACCTACCAATGCGGCTCCAGCTGCTGGCCATGCCAAGCCAGGG	1152
DB	1817	CGCTGCTCTCTGCTACCAATGCGGCTCCAGCTGCTGGCCATGCCAAGCCAGGG	1876
QY	1153	GCTCCAGCCACTGAGACTGAAACCTTACCAGTCACTATGCGGCTTCCCAGGACGATGGA	1212
DB	1877	GCTCCAGCCACTGAGAACCAACATACCAGTTACTATGACAGTTCCCAAGGACGAGCG	1936
QY	1213	TTCTTAAAGGCTCTGCTCAGGCTTGGATGAGGAGGCTTCCGGGTCTGGCGCGGCGCT	1272
DB	1937	TTCTTAAAGGCTCTGCTCAGGCTTGGATGAGGAGGCTTCTGGGTCTGGCGGCGCACCT	1996
QY	1273	CAATTGTCAGGAAGATGGGAAACAGTCACTGACTGGGCACTAGG	1320
DB	1997	CAATTGTCAGGAAGATGGGAAACAGTCACTGACTGGGCACTAAG	2044

RESULT 8

MMHPRP	1984 bp	mRNA	linear	ROD 04-MAY-1994
LOCUS	M.musculus mRNA for parathyroid hormone/parathyroid hormone related peptide receptor.			
DEFINITION	peptide receptor.			
ACCESSION	X78936			
VERSION	X78936.1 GI:474828			
KEYWORDS	G-protein coupled receptor; parathyroid hormone; parathyroid hormone related peptide receptor; parathyroid hormone-related protein.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 Karperien, M., Van Diik, T.B., Hoeijmakers, T., Cremers, F., Abou-Samra, A.B., Boonstra, J., De Laat, S.W. and Defize, L.H.K.			
TITLE	Expression pattern of parathyroid hormone/parathyroid hormone related peptide receptor mRNA in mouse postimplantation embryos indicates involvement in multiple developmental processes			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 1984)			
AUTHORS	Karperien, M.			

sequence		Location/Qualifiers	
FH	Key	(1)..(1347)	
FT	CDS		
FEATURES		Location/Qualifiers	
source		1..1363	
		/organism="synthetic construct"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:32630"	
ORIGIN			
Query Match		74.5%; Score 983.8; DB 6; Length 1363;	
Best Local Similarity		84.8%; Pred. No. 5.4e-195;	
Matches 1153; Conservative		0; Mismatches 167; Indels 39; Gaps 3;	
Qy	1	ATGGGGCGCCCGGATCGACCCAGCCTGCGCTCTTACTCTGCTGCCAGTGTCTCAGC	60
Db	1	ATGGGACCGCCCGGATCGACCCCGCCTGGCGTCTCTGCTGCTGCCCGTGTCTCAGC	60
Qy	61	TCCGATATGCGCTG-----GAGGTATTGAC	87
Db	61	TCCGCTACGGCGTTTCGAAATCCAGCTGATGCACGCGGAGGCGAGGTGTTTAC	120
Qy	88	CGCTTAGCATGATCTACACGCTGGGATCTCCATGCTCTCGCTCCCTCACGGTGGCT	147
Db	121	CGCTGGGCATGATTTACACGCTGGGCTACTCCGTGCTCCTGGCGTCCCTCACGTAGCT	180
Qy	148	GTGCTCATCTCGGCCTATTTTAGCGGCTGCACCTGCACGCGCAACTACATCCATGCAC	207
Db	181	GTGCTCATCTCGGCCTACTTTAGCGGCTGCACCTGCACGCGCAACTACATCCATGCAC	240
Qy	208	ATGTTCTGTGTTATGCTGGCGCGCGAGCATCTTCGTGAAGAGCGCTGTGCTTAC	267
Db	241	CTGTCTCTGCTTCTATGCTGGCGCGCGTGGAGCATCTTCGTCAAGGACGCTGTGCTTAC	300
Qy	268	TCTGGCTTCAGCTGATGAGCGCGAGCGCTCTCAGAGGAGAGTTCGCATCATCGCG	327
Db	301	TCTGGCGCACGCTTGATGAGGCTGAGCGCTCTCAGAGGAGAGTGGCGCCATCGCC	360
Qy	328	CAGGTGCCACCTCGCGCGCGCTGCGCGCTAGGCTACGCTGGCTGGCGCTGGCGGTG	387
Db	361	CAGGCGCGCGCGCTGCCACCGCGCTGCGGCTACGCGGCTGCAGGGTGGCTGTG	420
Qy	388	ACCTTCTCTCTACTTCTGGCTACCACTACTGATCTGATCTGCTGGAGGGGCTGTAC	447
Db	421	ACCTTCTCTTACTTCTGGCTACCACTACTGATCTGATCTGCTGGAGGGGCTGTAC	480
Qy	448	TTCACAGCTCATCTTATGCTGCTTTTCTCAGAGAGAGTACCTTGGGGCTTCACC	507
Db	481	CTGCACAGCTCATCTTATGCTGCTTTCTCAGAGAGAGTACCTTGGGGCTTACA	540
Qy	508	ATCTTTGGCTGGGCTTACCGGCTGTCTCGTGGCTGTGGGTGGGTTCAGAGCAACC	567
Db	541	GTCTTGGCTGGGCTTACCGGCTGTCTCGTGGCTGTGGGTGGGTTCAGAGCTTACC	600
Qy	568	TGGCCAACTCTGGGTCTGGGATCTGAGCTCCGGGCAACAAGTGGATCATCCAGTG	627
Db	601	CTGGCCAACTCTGGGTCTGGGATCTGAGCTCCGGGCAACAAGTGGATCATCCAGTG	660
Qy	628	CCATCTCGGATCTGTTGTGCTCAACTTCATCTCTTTTATCAATCATTCGGGTGCTT	687
Db	661	CCATCTCGGCTTCCATTTGCTCAACTTTCATCTCTTTCATCAATCATTCGGGTGCTC	720
Qy	688	GCCACTAGCTTCGGGAGACCAATGCGGCGGCTGTGACACAGCAGCAGTACCGGAAG	747
Db	721	GCCACCAAGCTTCGGGAGACCAACGCGCGCGGTGTGACACGCGCAGTACCGGAAG	780
Qy	748	CTGCTCAGGTCCAGTGTGGTGTCTGTCGCGCTCTTTGGTGTGCACTACACCGTCTTATG	807
Db	781	CTGCTCAATCCAGCTGGTGTCTCATGCCCTCTTTGGCGTCCACTACATTTGCTTATG	840
Qy	808	GCCTTGGCGTACACCGAGGTCTCAGGAGCATTTGTGGCAGATCCAGATGATGAGATG	867
Db	841	GCCACCATACACCGAGGTCTCAGGAGCGCTCTGGCAAGTCCAGATGCACTATGAGATG	900

Qy	868	CTCTTCAACTCTCTCCAGGGATTTTTTGTGGCATCATATACTGTTTCTGCAATGGTGAG	927
Db	901	CTCTTCAACTCTCTCCAGGGATTTTTTGTGCGCAATCATATATACTGTTTCTGCAATGGCGAG	960
Qy	928	GTGCAAGCAGAGATTAGGAAGTCATGGAGCGCTCGACACTGGCGTTTGGACTTCAAGGCGC	987
Db	961	GTACAAAGCTGAGATCAAGAAATCTTTGGAGCCGCTGGACACTTGGCACTGAGACTTCAAGGCA	1020
Qy	988	AAAGCACGAAGTGGGAGTAGCAGCTACAGCTATATGCCCCTTCTTCTCACACGAGTGTG	1047
Db	1021	AAAGCAGCAGCGGAGCAGCAGCTATAGTACGCGCCCATGTTCTCCACACAAAGTGTG	1080
Qy	1048	ACCAATGTGGGCGCCCGGTGACGAGACTCAGCCTCCCGCTCAGCCCGCGC---CTGGCTCTCT	1104
Db	1081	ACCAATGTGGGCGCCCGGTGTGGGACTCGGCGCTTGGCGCTTCCAGCCCGCGCTACTGCCCCACT	1144
Qy	1105	GCCACTTACCAATGGCCACTCCCGAGCTGCTGCGCATGCCAAGCAGCGGGCTCCAGCCACT	1166
Db	1141	GCCACCAACACGGCCACCTCAGCTGCTGCGCATGCGAAGCAGGACCCAGCCGCTG	1200
Qy	1165	GAGAC---TGAACCCCTACAGTCACTATGGCGGTTCACAGGACGATGGATTCCTTAAC	1222
Db	1201	GAGACCTCGAGACCAACACCACTCGCATGGCTGCTCCCAAGGACGATGGGTTCCTCAAC	1260
Qy	1222	GGCTCTGCTCAGGCTGTGATGAGAGGCTCTCGGCTCTGCGCGCGCGCTTCCATTTGTG	1288
Db	1261	GGCTCTGCTCAGGCTGTGACGAGGAGGCTCTGCGCGCTGAGCGGCCACCTGCCCTGCTA	1320
Qy	1282	CAGGAGGATGGGAACAGTCACTGATGCGGCACCTAGG	1320
Db	1321	CAGGAAGAGTGGGAGACAGTCACTGACCAAGCGCTGGG	1359

RESULT 11	BD266845	1380 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.				
DEFINITION	BD266845				
ACCESSION	BD266845				
VERSION	1 GI:33076613				
KEYWORDS	JP 2002533115-A/14.				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 1380)				
AUTHORS	Gardella, T.J., Kronenberg, H.M., Potts, J.T. and Jueppner, H.				
TITLE	PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules				
JOURNAL	Patent: JP 2002533115-A 14 08-OCT-2002; THE GENERAL HOSPITAL CORP				
COMMENT	OS Artificial Sequence				
	PN	JP 2002533115-A/14			
	PD	08-OCT-2002			
	PF	30-DEC-1999 JP 2000591171			
	PR	31-DEC-1998 US 60/114577			
	PI	THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI JUEPPNER			
	PC	C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P5/18, A61P19/08, P1 A61P19/10,			
	PC	A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, C12N1/21,			
	PC	C12N5/10, G01N33/15, G01N33/50, C12N15/00, C12N15/00, A61K37/02 CC			
	Description of Artificial Sequence: modified PTH receptor CC				
	sequence				
FH	Key	Location/Qualifiers			
FT	CDS	(1)..(1353).			
FEATURES		Location/Qualifiers			
source		1..1380			
		/organism="synthetic construct"			
		/mol_type="genomic DNA"			
		/db_xref="taxon:32630"			
ORIGIN					

RESULT 11

BD266845

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PF

PI

JUEPPNER

PC

A61P19/10,

PC

PC

PC

Description of Artificial Sequence: modified PTH receptor CC

FH

FT

CDS

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1..1380

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

source

FEATURES

sequence

Location/Qualifiers

1

Query Match 74.1%; Score 977.8; DB 6; Length 1380;
Best Local Similarity 84.5%; Pred. No. 9.7e-194; Indels 45; Gaps 3;
Matches 1153; Conservative 0; Mismatches 167;

Qy 1 ATGGGGGCGCGCCGGATCGCACCCAGGCTCGCGCTCTCTACTCTGCTGCCAGCTGCTCAGC 60
Db 1 ATGGGGACCGCGCCGGATCGCACCCGGCTGGCGCTCTGCTCTGCTGCTGCCCGCTGCTCAGC 60

Qy 61 TCCGCATATGGCGTG-----GAGGTA 81
Db 61 TCCGCGTACGCGGTTTCGAAATCCAGCTGATGCATAATCGTGGCGGAGGCGAGGTG 120

Qy 82 TTTGACCGCTAGCATGATCTACACCGTGGATCTCCATGCTCTCGCTCCCTCCACG 141
Db 121 TTTGACCGCTGGGCATGATTTACACCGTGGCTACTCCGCTGCTCCCTGGCGTCCCTCACC 180

Qy 142 GTGCTGTGCTCATCTCGGCTATTTAGCGGCTGCACCTGCAGCGCAACTACATCCAC 201
Db 181 GTAGCTGTGCTCATCTCGGCTACTTTAGCGGCTGCACCTGCAGCGCAACTACATCCAC 240

Qy 202 ATGACATGTTCTGCTGTTTATGCTGGCGCCCGAGCATCTTCTGTTGAAGGACGCTGTG 261
Db 241 ATGACACCTGTTCTGCTCTCATGCTCGCGCCGCTGAGCATCTTCTGTTCAAGGACGCTGTG 300

Qy 262 CTCTACTCTGGCTTCAGCGTGGATGAGCGCGAGCGCTCCACAGGAGAGTTCGCATC 321
Db 301 CTCTACTCTGGCGCACGCTTGATGAGCTGAGCGCTCACCGAGGAGAGCTGCGCGCC 360

Qy 322 ATCGCGAGGTGCCACCTCTCGCGCGCGCTGCCCGCTGAGCTACGCTGGCTGCGCGGTG 381
Db 361 ATCGCGCAGCGCGCGCGCGCTGCCACCGCGCTGCGCGCTACGCGGCTGCAGGGTG 420

Qy 382 GCGGTGACCTTCTTCTCTACTTCTGCTGCTACCACTACTCTGATCTCTGCTGGAGGGG 441
Db 421 GCTGTGACCTTCTTCTTCTTCTCTGCTGCCACCACTACTCTGATCTCTGCTGGAGGGG 480

Qy 442 CTGTACTTGCACGCTCANTCTCATGCGCTTTTCTCAGAGAGAGTACCTGTGGGC 501
Db 481 CTGTACTTGCACGCTCANTCTCATGCGCTTTTCTCAGAGAGAGTACCTGTGGGC 540

Qy 502 TTCAACCATCTTTGCTGGGCTTACCGGCTGTCTTCGTTGGCTGTGTTGGCTGTCGAGT 561
Db 541 TTCAAGCTTTCGCTGGGCTGCGCGCTGCTCTTCGTTGGCTGTGTTGGCTGTCGAGT 600

Qy 562 GCACCTTTGGCCAACTCTGGGTGCTGGGATCTGAGCTCCGGGCAACAAGATGATCATC 621
Db 601 GCTACCTTGGCCAACTCTGGGATCTGGGACTTGGCTCCGGGCAACAAGATGATCATC 660

Qy 622 CAGTGCCCATCTCGGCATCTGTTGTGCTCAACTTCACTCTTTTATCAACATCATCCGG 681
Db 661 CAGTGCCCATCTCGGCCTCAATGTGCTCAACTTCACTCTTTTATCAATATCTGTCGG 720

Qy 682 GTGCTTGCCTAAGCTTTCGGGAGACCAATGCGGGCGGCTGTGACACAGGACGAGTAC 741
Db 721 GTGCTTGCCTAAGCTTTCGGGAGACCAACGCGCGCGGCTGTGACACAGGACGAGTAC 780

Qy 742 CGGAAGCTGTCAAGTCCAGTTCAGTTCGCTGCTGCGCTCTTTTGTGTCATCAACCGTC 801
Db 781 CGGAAGCTGTCAAAATCCAGCTGGTGTCTATGCTCCCTCTTTGGCGTCCACTATGTC 840

Qy 802 TTTGATGGCTTGGCTACACCGAGTCTCAGGACATTTGGACATTTGGACATTCAGATGCA 861
Db 841 TTTGATGGCCACCATACACCGAGTCTCAGGAGACGCTCTGGCAAGTCCAGATGCACTAT 900

Qy 862 GAGATGCTTTCAACTCTCTCCAGGATTTTTTGTGTCATCATATATCTGTTCTGCAAT 921
Db 901 GAGATGCTTTCAACTCTCTCCAGGATTTTTTGTGTCATCATATATCTGTTCTGCAAT 960

Qy 922 GGTGAGGTGACGAGCAGATTTAGAACTCATGAGCGCTGGAACACTGCGGCTTGGACTTC 981
Db 961 GGCAGGGTACAAAGCTGAGATCAAGAAATCTTTGAGCGCTGGACACTGCGCACTGGACTTC 1020

982 AAGCGCAAGCACAAAGTGGAGTAGCAGTACAGCTATATGGCCCAATGGTGTCTCACACG 1041
Db 1021 AAGCGAAAGCAGCAGCGGAGCAGCAGTATAGTACGGCCCATGGTGTCTCCACACA 1080

Qy 1042 AGTGTACCAATGTGGGCCCCCGTGCAGGACTCAGCTCCCTCCCTCAGCCCCCGC---CTG 1098
Db 1081 AGTGTACCAATGTGGGCCCCCGTGTGGGACTCGGCTCGGCTCAGCCCCCGCCTACTG 1140

Qy 1099 CTCTCTGCCATACCAATGGCCACTCCAGCTGCCCTGGCCATGCCAAGCAGGGGTCCA 1158
Db 1141 CCACCTGCCACCAACCGCCACCTCAGCTGCTGGCCATGCCAAGCAGGGAGCCCCA 1200

Qy 1159 GCCACTGAGAC---TGAAACCCCTACCAGTCACTATATGGCGGTTCCCAAGACGATGATTC 1215
Db 1201 GCCTTGGAGACCTTCAGACCAACACCTGCTGCTGCCATGGCTGCCAAGACGATGGTTC 1260

Qy 1216 CTTAACGGCTCTCTGCTCAGGCTTGGATGAGGAGGCTTCGGGCTCTCGCGGCGCTCCA 1275
Db 1261 CTCAACGGCTCTCTGCTCAGGCTTGGACGAGGAGGCTCTGGGCTGAGCGGCCACCTGCC 1320

Qy 1276 TTGTTCCAGGAGGATGGGAAACAGTCACTGATGCTGGGCACTAGG 1320
Db 1321 CTGCTACAGGAGAGTGGGAGACAGTCACTGTGACGAGCGCTGGG 1365

RESULT 12
BD266837
LOCUS
DEFINITION
BD266837
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD266837 975 bp DNA linear PAT 17-JUL-2003
PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules.
BD266837
BD266837.1 GI:33076605
JP 2002533115-A/6.
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 975)
Gardella, T.J.; Kronenberg, H.M., Potts, J.T. and Jueppner, H.
PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules
Patent: JP 2002533115-A 6 08-OCT-2002;
THE GENERAL HOSPITAL CORP
OS Artificial Sequence
PN JP 2002533115-A/6
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591171
PR 31-DEC-1998 US 60/114577
PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI
JUEPPNER
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P5/18, A61P19/08, PC
A61P19/10,
PC A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, G01N33/15, G01N33/50, C12N15/00, C12N5/00, A61K37/02 CC
Description of Artificial Sequence: modified PTH receptor CC
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
1..975
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
ORIGIN

Query Match 73.7%; Score 973.4; DB 6; Length 975;
Best Local Similarity 99.9%; Pred. No. 8.3e-193;
Matches 974; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGGGCGCGCCGGATCGCACCCAGCTGCGGCTCTCTACTCTGCTGCCAGTGTCTCAGC 60
Db 1 ATGGGGGCGCGCCGGATCGCACCCAGCTGCGGCTCTCTACTCTGCTGCCAGTGTCTCAGC 60


```
VERSION AX548943.1 GI:25813781
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burner, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 228 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
source
1. 1948
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 73.2%; Score 966.8; DB 6; Length 1948;
Best Local Similarity 86.6%; Pred. No. 1.9e-191;
Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;
Qy 69 TGGCTGGAGATATTGACCGCCTAGGATGATCTACACGGTGGGATACCTCATGTCTCT 128
Db 565 TGAACGGGAGGTGTTGACCGCCTGGGATGATTTACACCGTGGGCTACTCCGTGTCCT 624
Qy 129 CGCTCCCTCAGCTGCTGCTCATCTCCGCTATTTAGGGGCTGCACTGCACGCG 188
Db 625 GGCCTCCCTCACCCTAGCTGCTGCTCATCTCCGCTACTTTAGGGGCTGCACTGCACGCG 684
Qy 189 CAATACATCACAATGACATGTTCTGCTGCTTTATGCTGCGCCCGGAGCATCTTTCGT 248
Db 685 CAATACATCACAATGACATGTTCTGCTGCTTTATGCTGCGCCCGGAGCATCTTTCGT 744
Qy 249 GAAGGAGCTGTGCTTACTCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 308
Db 745 CAAGGAGCTGTGCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
Qy 309 AGAGTTCACATCATCGGAGGTCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 368
Db 805 GGAGCTGCGGCCATCGGAGGTCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
Qy 369 TGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
Db 865 GGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924
Qy 429 CTTGGTGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
Db 925 TCTGGTGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
Qy 489 GTACTGTGGGCTTCAACCATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
Db 985 GTACTGTGGGCTTCAACCATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
Qy 549 GGTGGTGTGAGGAACTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
Db 1045 GGTGAGTGTGAGGCTTACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104
Qy 609 GAAGTGGATCATCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
Db 1105 AAAGTGGATCATCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
Qy 669 CAACATCATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
Db 1165 CAATATCATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
Qy 729 CAGGACAGGTACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Db 1225 ACGGACAGGTACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1284
Qy 789 GCACTACACCGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
```

```
Db 1285 CCACATCATGTTCTTATGCGCCACACCATACCGAGGTCTCAGGGGACGCTCTGCGCAAGT 1344
Qy 849 CCAGATGCATTATGAGATGCTCTTCACTCTCTTCCAGGGGATTTTGTGTCATCATATA 908
Db 1345 CCAGATGCATTATGAGATGCTCTTCACTCTCTTCCAGGGGATTTTGTGTCATCATATA 1404
Qy 909 CTGTTTCTGCAATGGTGGTGGTGGGAGAGATTAGAAAGTCTATGGAGCGGCTGGACACT 968
Db 1405 CTGTTTCTGCAATGGGAGGATCAAGCTGAGATCAAGAAATCTTGGAGCGGCTGGACACT 1464
Qy 969 GCGTTTGGACTTCAAGCGCAAGCAAGAGTGGGAGTAGCAGCTACAGCTATGCGCCCAAT 1028
Db 1465 GGCATGAGACTTCAAGCGAAAGGACGACGCGGAGCAGCAGCTATAGCTACGCGCCCAT 1524
Qy 1029 GGTGTCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGAGCTCAGCCCTCCCCCTCAG 1088
Db 1525 GGTGTCCACACAGTGTGACCAATGTGGGCCCCCGTGTGGAGCTCGGCCCTGCCCCCTCAG 1584
Qy 1089 CCCCCGC---CTGCTCTCTGCCACTACCAATGGGCACTCCAGCTGCTGCGCCATGCCAA 1145
Db 1585 CCCCCGCCTACTGCTCCACTGCTCACCACCAACGCGCCACCTCAGCTGCTGCGCCATGCCAA 1644
Qy 1146 GCCAGGGGCTCCAGCCCACTGAGAC---TGAACCTTACCAGTCACTATGGGGTTCCCAA 1202
Db 1645 GCCAGGAGACCCAGCCCTGGAGACCTTCGAGACCAACACCACTGCTGCTGCTGCCAA 1704
Qy 1203 GAGCATGAGATTCTTAAACGGCTCTGCTCAGGGCTGGATGAGGAGGCTCCCGGCTCTGC 1262
Db 1705 GAGCATGAGATTCTTAAACGGCTCTGCTCAGGGCTGGATGAGGAGGCTCTGCGGCTGA 1764
Qy 1263 GCGGCGGCTTCCATTTGTCAGGAAGGATGGGAAACAGTCACTGCTGCGGCACTAGG 1320
Db 1765 GCGGCGGCTTCCATTTGTCAGGAAGGATGGGAGACAGTCACTGCTGCGGCACTAGG 1822
```

Search completed: July 4, 2005, 01:28:06
Job time : 5924 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 15:10:00 ; Search time 788 Seconds
(without alignments)
9916.318 Million cell updates/sec

Title: US-09-869-565-1

Perfect score: 1320

Sequence: 1 atggggccgcgcggatgcg.....tcattgactgggcaactagg 1320

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1320	100.0	1320	3	AAA58932 DNA encod
2	1260.2	95.5	1341	3	AAA51732 Tethered
3	1243.2	94.2	2051	2	AAT15947 Rat bone
4	1243.2	94.2	2051	2	AAV08390 Parathyro
5	1243.2	94.2	2051	12	ADH61258 Rat bone
6	1241.6	94.1	2065	10	ABT42039 Toxicity
7	1240	93.9	2051	2	AAQ29606 Rat bone
8	1146.4	86.8	1776	12	ADO30323 Mouse GPC
9	1006.4	76.2	1380	3	AAA51736 Human tet
10	982.2	74.4	1363	3	AAA51735 Human tet
11	979.4	74.2	1380	3	AAA51737 Human tet
12	973.4	73.7	975	3	AAA51734 Tethered
13	966.8	73.2	1948	8	ABZ42719 Human par
14	966.8	73.2	1948	10	ACA56655 Human sig
15	966.8	73.2	1948	10	ADL13887 Osteoarth
16	966.8	73.2	1948	10	ADL13875 Osteoarth
17	966.8	73.2	1948	12	ADI56451 Human pol
18	966.8	73.2	1948	13	ADR47543 Human par
19	966.8	73.2	2282	12	ADQ22747 Human sof
20	965.2	73.1	2010	2	AAV08391 Human Par

21	965.2	73.1	2010	12	ADH61259	Adh61259 Human PTH
22	965.2	73.1	2171	10	ADD71008	Add71008 Human par
23	965.2	73.1	2171	12	ADQ18188	Adq18188 Human sof
24	962	72.9	2010	2	AAT15948	Aat15948 Human kid
25	961.2	72.8	1782	10	ADL13876	Adl13876 Osteoarth
26	961.2	72.8	1782	10	ADL13886	Adl13886 Osteoarth
27	961.2	72.8	1785	12	ADQ76824	Adq76824 Human wil
28	959.6	72.7	1782	5	ABI98021	Abi98021 Non-endo
29	959.6	72.7	1782	12	ADO30033	Ado30033 Human GPC
30	958.2	72.6	1779	10	ADF70391	Adf70391 Human PTH
31	946.2	71.7	2006	2	AAQ29607	Aaq29607 Human kid
32	925.6	70.1	1008	3	AAA51733	Aaa51733 Tethered
33	902.2	68.3	2177	8	ABX15515	Abx15515 cDNA enco
34	691.6	52.4	1863	2	AAT15946	Aat15946 Opossum k
35	691.6	52.4	1863	2	AAV08389	Aav08389 Parathyro
36	691.6	52.4	1863	12	ADH61257	Adh61257 Opossum k
37	690	52.3	1863	2	AAQ29605	Aaq29605 Opossum k
38	681.2	51.6	1862	2	AAT15945	Aat15945 Opossum k
39	681.2	51.6	1862	2	AAV08388	Aav08388 Parathyro
40	681.2	51.6	1862	12	ADH61256	Adh61256 Opossum k
41	678	51.4	1862	2	AAQ29604	Aaq29604 Opossum k
42	554.6	42.0	1609	3	AAA30828	Aaa30828 Zebrafish
43	554.6	42.0	1609	3	AAA49625	Aaa49625 Zebrafish
44	554.6	42.0	1609	10	ADC42304	Adc42304 cDNA enco
45	554.6	42.0	1609	10	ADH61058	Adh61058 Zebrafish

ALIGNMENTS

RESULT 1

AAA58932

ID AAA58932 standard; DNA; 1320 BP.

XX AC AAA58932;

XX DT 20-OCT-2000 (first entry)

DE DNA encoding a mutant parathyroid hormone (PTH) receptor.

KW Mutant; parathyroid hormone; PTH; receptor; rdeltant;

KW ligand binding domain; ss.

XX OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..1308

FT sig_peptide /*tag= a

FT /*tag= b

FT mat_peptide 67..1305

FT /*tag= c

XX WO200040698-A1.

PN 13-JUL-2000.

PD 31-DEC-1998; 98WO-US027862.

PF 31-DEC-1998; 98WO-US027862.

PR 31-DEC-1998; 98WO-US027862.

PA (GEHO) GEN HOSPITAL CORP.

XX Gardella TJ, Kronenberg HM, Potts JT;

XX WPI; 2000-465971/40.

DR P-PSDB; AAB07529.

XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a

PT deletion of the extracellular amino-terminus ligand binding domain,

PT useful in screening assays for identifying agonists and antagonists of

PT PTH receptor activity.

XX

Claim 2; Fig 1; 81pp; English.

xx CC The present sequence encodes a mutant parathyroid hormone (PTH) receptor,
CC designated rdclant. The polypeptide is characterised by a deletion of
CC the extracellular amino-terminus ligand binding domain. The receptor has
CC a minimal domain for ligand binding and is, therefore, useful in
CC screening assays designed for the identification of agonists and
CC antagonists of PTH receptor activity

Sequence 1320 BP; 238 A; 402 C; 373 G; 307 T; 0 U; 0 Other; XX

Query Match	100.0%;	Score 1320;	DB 3;	Length 1320;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1320;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy	1	ATGGGGCGCGCCCGATCGCAACCGAGCTGGGGCTCTTACTCTGTGTGCCCATGTGCTCAGC	60
Db	1	ATGGGGCGCGCCCGATCGCAACCGAGCTGGGGCTCTTACTCTGTGTGCCCATGTGCTCAGC	60
Qy	61	TCGCGATATGGCTGGAGGATTTGACCGCTAGGCATGATCTACACCGTGGGATACATCC	120
Db	61	TCGCGATATGGCTGGAGGATTTGACCGCTAGGCATGATCTACACCGTGGGATACATCC	120
Qy	121	ATGTCTCTCGCCTCCCTCACGGTGGCTGTGCTCATCTCGGCTATTTTAGCGGGCTGCAC	180
Db	121	ATGTCTCTCGCCTCCCTCACGGTGGCTGTGCTCATCTCGGCTATTTTAGCGGGCTGCAC	180
Qy	181	TGCACGGCAACTACATCCACATGATGTTCTCTGTCTGCTGTTATGTCTGGCGCGCGAGC	240
Db	181	TGCACGGCAACTACATCCACATGATGTTCTCTGTCTGCTGTTATGTCTGGCGCGCGAGC	240
Qy	241	ATCTTCGTGAAGGACGCTGTGCTCTACTCTGCTTACGCTGGATAGCGCCAGCGCCTC	300
Db	241	ATCTTCGTGAAGGACGCTGTGCTCTACTCTGCTTACGCTGGATAGCGCCAGCGCCTC	300
Qy	301	ACAGAGGAAGTGTGCACATCATCGCGAGGTGCCACCTCCGCGCGCGCTGCCGCCGTA	360
Db	301	ACAGAGGAAGTGTGCACATCATCGCGAGGTGCCACCTCCGCGCGCGCTGCCGCCGTA	360
Qy	361	GGCTACGCTGGCTGGCGGTGACACTTCTTCTCTACTCTTCTTCTACTCTTATGGCCTTTTCTCA	420
Db	361	GGCTACGCTGGCTGGCGGTGACACTTCTTCTCTACTCTTCTTCTACTCTTATGGCCTTTTCTCA	420
Qy	421	TACTGGATCCTGTGGAGGGCTGTACTTGCACAGCCTCATCTTACATGCGCCTTTTCTCA	480
Db	421	TACTGGATCCTGTGGAGGGCTGTACTTGCACAGCCTCATCTTACATGCGCCTTTTCTCA	480
Qy	481	GAGAGAAGTACTCTGTGGGGCTTACCATTCTTTGGCTGGGGTCTACCGGGCTGTCTTCGTG	540
Db	481	GAGAGAAGTACTCTGTGGGGCTTACCATTCTTTGGCTGGGGTCTACCGGGCTGTCTTCGTG	540
Qy	541	GCTGTGGGTGGTGTGAGAGCAACCTTTGGCGCAACCTGTGGGTGTGGGATCTGAGCTCC	600
Db	541	GCTGTGGGTGGTGTGAGAGCAACCTTTGGCGCAACCTGTGGGTGTGGGATCTGAGCTCC	600
Qy	601	GGGCACAAGAGTGGATCATCCAGGTGCCATCCTGGGCATCTGTGTGCTCAACTCATC	660
Db	601	GGGCACAAGAGTGGATCATCCAGGTGCCATCCTGGGCATCTGTGTGCTCAACTCATC	660
Qy	661	CTTTTTATCAACATCATCCGGGTGCTTCCCACTAAGCTTTCGGGAGACCAATTCGGGGCGG	720
Db	661	CTTTTTATCAACATCATCCGGGTGCTTCCCACTAAGCTTTCGGGAGACCAATTCGGGGCGG	720
Qy	721	TGTGACACCGGACGAGTACCGGAAGCTGTCTAGGTCCAGTTGGTGTCTGTCCGCTC	780
Db	721	TGTGACACCGGACGAGTACCGGAAGCTGTCTAGGTCCAGTTGGTGTCTGTCCGCTC	780
Qy	781	TTTTGGTGTGCACTACACCGTCTTATGCGCTTCCGCTACCGAGGTCTCAGGGACATTG	840
Db	781	TTTTGGTGTGCACTACACCGTCTTATGCGCTTCCGCTACCGAGGTCTCAGGGACATTG	840
Qy	841	TGGCAGATCCAGATGCATTATGAGATGCTCTTCAACTCTTCCAGGGATTTTTTTTGTGCC	900

PR 05-APR-1991; 91US-00681702.
XX (GEHO) GEN HOSPITAL CORP.
PA Potts JT, Juppner H, Segre GV, Schipani E, Kronenberg HM;
PI Abou-Samra A;
XX MPI; 1996-139028/14.
DR P-PSDB; AAR92277.
XX
XX DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia, cancer
PT etc.
XX
XX Claim 1; Fig 3A-3E; 64pp; English.
XX
XX A cDNA clone (AAT15947), designated R15B ATCC 68571, codes for a rat
CC parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
CC receptor (AAR92277). To obtain R15B, a rat osteosarcoma ROS 17/2.8 cDNA
CC library in pcDNA1 was used to transfect COS cells, and transfectants were
CC selected for ability to bind labelled PTH. Recombinant receptor is
CC produced in vector/host cell systems. The host cells can be used for
CC diagnostic measurement of PTH serum levels. Transgenic chickens that
CC overexpress the receptor in their oviduct lay eggs of higher calcium
CC content. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;
SQ
Query Match 94.2%; Score 1243.2; DB 2; Length 2051;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
73 CTGAGGATTTTGACCCCTAGGATGATCTACACCGTGGGATCTCCATGCTCTCGCC 132
613 CGGAGGATTTTGACCCCTAGGATGATCTACACCGTGGGATCTCCATGCTCTCGCC 672
133 TCCCTCAGCGTGGCTGCTCATCTCGCTCTATTTTAGGCGGCTGCACTCAGCGCAAC 192
673 TCCCTCAGCGTGGCTGCTCATCTCGCTCTATTTTAGGCGGCTGCACTCAGCGCAAC 732
193 TACATCCACATGACATGTTCTCTGCTGCTTTATGCTGCGCCGCGAGCATCTTCGTGAAG 252
733 TACATCCACATGACATGTTCTCTGCTGCTTTATGCTGCGCCGCGAGCATCTTCGTGAAG 792
253 GACGCTGTCTTACTCTGCTTTCAGCTGATGAGCGCCGAGCGCTTCACAGGAGAGAG 312
793 GACGCTGTCTTACTCTGCTTTCAGCTGATGAGCGCCGAGCGCTTCACAGGAGAGAG 852
313 TTGCACATCATCGCGCAGGTGACACCTCCGCGCGCGCTGCGCGGTAGGCTACGCTGGC 372
853 TTGCACATCATCGCGCAGGTGACACCTCCGCGCGCGCTGCGCGGTAGGCTACGCTGGC 912
373 TGGCGGTGCGGTGACCTTCTCTCTACTTCTGCTTACCACTACTACTGATCTG 432
913 TGGCGGTGCGGTGACCTTCTCTCTACTTCTGCTTACCACTACTACTGATCTG 972
433 GTGAGGGGCTGTACTTGCACAGGCTCATCTTCATGCGCTTTTCTCAGAGAGAGTAC 492
973 GTGAGGGGCTGTACTTGCACAGGCTCATCTTCATGCGCTTTTCTCAGAGAGAGTAC 1032
493 CTGTGGGGCTTACCATCTTTGGCTGGGGCTACCGGCTGTCTTGGGGCTGTGGGTC 552
1033 CTGTGGGGCTTACCATCTTTGGCTGGGGCTACCGGCTGTCTTGGGGCTGTGGGTC 1092
553 GGTGTACAGAACCTTTGGCCAAACACTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 612
1093 GGTGTACAGAACCTTTGGCCAAACACTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 1152
613 TGGATCATTCAGGTGCGCATCTGTTGCTGCTCACTCATCTCTTTTATCAAC 672
1153 TGGATCATTCAGGTGCGCATCTGTTGCTGCTCACTCATCTCTTTTATCAAC 1212
673 ATATCCGGGTGCTTGGCACTTAAGCTTTCGGGAGACCAATGCGGCGCGGTGTGACACCAAGG 732

RESULT 4

AAV08390

ID AAV08390 standard; DNA; 2051 BP.

XX AAV08390;

XX AC AC (first entry)

XX DT 08-FEB-1999

XX DE Parathyroid hormone receptor R15B coding sequence.

XX DE Parathyroid hormone receptor; PTH receptor; antibody; therapy;

XX KW PTH-related hypercalcaemia; rat; ds.

XX XX Rattus sp.

XX Key Location/Qualifiers

XX CDS 73..1848

XX FT /*tag= a

XX XX US5840853-A.

XX PD 24-NOV-1998.

XX PF 06-JUN-1995; 95US-00471494.

XX XX 05-APR-1991; 91US-00681702.

XX PR 06-APR-1992; 92US-00864475.

XX XX (GEHO) GEN HOSPITAL CORP.

XX Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;
PI Kronenberg HM;
XX WPI; 1999-034124/03.
XX P-PSDB; AAW73316.
XX Antibody to parathyroid hormone receptor - for diagnostic or therapeutic
PT use.
XX Claim 6; Fig 3; 63pp; English.
XX This sequence encodes the rat parathyroid hormone (PTH) receptor R15B,
CC which is targeted by the antibody of the invention. The antibody of the
CC invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia
XX SQ Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;
Query Match 94.2%; Score 1243.2; DB 2; Length 2051;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 73 CTGAGGTATTGACCGCTAGGCGATGATACACCGTGGGATCTCCATGTCTCTCGCC 132
DB 613 CGGAGGTATTGACCGCTAGGCGATGATACACCGTGGGATCTCCATGTCTCTCGCC 672
QY 133 TCCCTCAGGTGGTGTGCTATCTCTGCTTTATTTAGGCGGTGCACTGACGCGCAAC 192
DB 673 TCCCTCAGGTGGTGTGCTATCTCTGCTTTATTTAGGCGGTGCACTGACGCGCAAC 732
QY 193 TACATCCACATGACATGTTCTCTGCTTTATGCTGCGCGCGAGCATCTTCGTGAAG 252
DB 733 TACATCCACATGACATGTTCTCTGCTTTATGCTGCGCGCGAGCATCTTCGTGAAG 792
QY 253 GACGCTGTGCTACTCTGGCTTCACTGAGTGGAGCGCGCTTACAGAGGAAGAG 312
DB 793 GACGCTGTGCTACTCTGGCTTCACTGAGTGGAGCGCGCTTACAGAGGAAGAG 852
QY 313 TTGCACATATCGCGGAGTGGACCTCCGCGCGCGCTGCGCGGTAGGCTAGCTGGC 372
DB 853 TTGCACATATCGCGGAGTGGACCTCCGCGCGCGCTGCGCGGTAGGCTAGCTGGC 912
QY 373 TGGCGGTGGCGGTGACCTTCTCTCTACTTCTGCTACCACTACTACTGATCTGTG 432
DB 913 TGGCGGTGGCGGTGACCTTCTCTCTACTTCTGCTACCACTACTACTGATCTGTG 972
QY 433 GTGAGGGGCTGTACTTTGCACAGCTTCACTTCAATGGCCCTTTTCTCAGAGGAAGTAC 492
DB 973 GTGAGGGGCTGTACTTTGCACAGCTTCACTTCAATGGCCCTTTTCTCAGAGGAAGTAC 1032
QY 493 CTGTGGGGCTTACCATCTTTGGCTGGGGTCTACCGGCTGTCTTGTGGCTGTGGGTC 552
DB 1033 CTGTGGGGCTTACCATCTTTGGCTGGGGTCTACCGGCTGTCTTGTGGCTGTGGGTC 1092
QY 553 GGTGTACAGCAACTTTGGCCCACTGGGTGCTGGGATCTGAGCTCGGGGCAACAAG 612
DB 1093 GGTGTACAGCAACTTTGGCCCACTGGGTGCTGGGATCTGAGCTCGGGGCAACAAG 1152
QY 613 TGGATCATCCAGGTGGCCCATCTGGCATCTGTTGTGCTCAACTTCATCTTTTATCAAC 672
DB 1153 TGGATCATCCAGGTGGCCCATCTGGCATCTGTTGTGCTCAACTTCATCTTTTATCAAC 1212
QY 673 ATCATCCGGGTGCTTGGCACTTAAGCTTGGGAGACCAATGCGGGCGGGTGTGACACAGG 732
DB 1213 ATCATCCGGGTGCTTGGCACTTAAGCTTGGGAGACCAATGCGGGCGGGTGTGACACAGG 1272
QY 733 CAGCAGTACCGGAGCTGCTCAGTTCACGTTGCTGCTGCGGCTCTTTGTGTGCAC 792
DB 1273 CAGCAGTACCGGAGCTGCTCAGTTCACGTTGCTGCTGCGGCTCTTTGTGTGCAC 1332

QY 793 TACACGCTCTTATGGCTTGGCGTACACCGAGGTCTCAGGAGCATTTGGCAGATCCAG 852
DB 1333 TACACGCTCTTATGGCTTGGCGTACACCGAGGTCTCAGGAGCATTTGGCAGATCCAG 1392
QY 853 ATGCAATTATGAGATGCTCTTCAACTCTCTCAGGATTTTTTTTGTGGCATCATATACTGT 912
DB 1393 ATGCAATTATGAGATGCTCTTCAACTCTCTCAGGATTTTTTTTGTGGCATCATATACTGT 1452
QY 913 TTCTGCAATGGTGAAGTGCAGGAGATTAGGAAGTTCATGGAGCGCTCGACACTGGCG 972
DB 1453 TTCTGCAATGGTGAAGTGCAGGAGATTAGGAAGTTCATGGAGCGCTCGACACTGGCG 1512
QY 973 TTGGACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1032
DB 1513 TTGGACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1572
QY 1033 TCTCACACGAGTGTGACCAATGTGGGCCCGCGTGCAGGACTCAGCCCTCCCGCTCAGCCCC 1092
DB 1573 TCTCACACGAGTGTGACCAATGTGGGCCCGCGTGCAGGACTCAGCCCTCCCGCTCAGCCCC 1632
QY 1093 CGCTGCTCTCTGCCACTACCAATGCCACTCCCGAGTGCCTGGCCATGCCAAGCCAGGG 1152
DB 1633 CGCTGCTCTCTGCCACTACCAATGCCACTCCCGAGTGCCTGGCCATGCCAAGCCAGGG 1692
QY 1153 GCTCCAGCCACTGAGACTGAAACCCCTACAGTCACTATGCGGTTCCCAAGAGCAGTGA 1212
DB 1693 GCTCCAGCCACTGAGACTGAAACCCCTACAGTCACTATGCGGTTCCCAAGAGCAGTGA 1752
QY 1213 TTCTTAAACGGCTCTGCTCAGGCTGGATGAGGAGCCCTCCCGGCTGCGCGGCCCT 1272
DB 1753 TTCTTAAACGGCTCTGCTCAGGCTGGATGAGGAGCCCTCCCGGCTGCGCGGCCCT 1812
QY 1273 CCATTGTTGAGGAAGGATGGGAAACAGTCACTGAGTGGGCACTAGG 1320
DB 1813 CCATTGTTGAGGAAGGATGGGAAACAGTCACTGAGTGGGCACTAGG 1860
RESULT 5
ADH61258
ID ADH61258 standard; cDNA; 2051 BP.
XX AC ADH61258;
XX DT 25-MAR-2004 (first entry)
XX DE Rat bone PTH/PTHrP receptor cDNA clone, R15B.
XX KW osteopathic; Parathyroid hormone receptor; hypercalcaemia;
XX KW hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
XX KW osseophagus multiple myeloma; hypocalcaemia; gene; cytostatic; rat; PTH;
XX PTHrP; PTH-related protein; ss.
XX OS Rattus rattus.
XX FH Key Location/Qualifiers
XX CDS 73..1848
XX FT /*tag= a
XX FT /product= "Rat bone PTH/PTHrP receptor protein"
XX XX US2003153041-A1.
XX PD 14-AUG-2003.
XX PF 09-OCT-2002; 2002US-00267730.
XX PR 05-APR-1991; 91US-00681702.
XX PR 06-APR-1992; 92US-00864475.
XX PR 06-JUN-1995; 95US-00471494.
XX PR 24-NOV-1998; 98US-00199874.
XX XX (GEO) GEN HOSPITAL CORP.
XX PA Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX PI

PR 01-NOV-2001; 2001US-0330867P.
PR 21-NOV-2001; 2001US-0331805P.
PR 06-DEC-2001; 2001US-0336144P.
PR 19-DEC-2001; 2001US-0340873P.
PR 21-FEB-2002; 2002US-0357842P.
PR 21-FEB-2002; 2002US-0357843P.
PR 21-FEB-2002; 2002US-0357844P.
PR 15-MAR-2002; 2002US-0364113P.
PR 08-APR-2002; 2002US-0370144P.
PR 08-APR-2002; 2002US-0370206P.
PR 17-APR-2002; 2002US-0370247P.
PR 17-APR-2002; 2002US-0372794P.
PR 21-APR-2002; 2002US-0371679P.
XX (GENE-) GENE LOGIC INC.
XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
XX WPI; 2003-148464/14.
XX
XX Predicting at least one toxic effect of a compound, useful for toxicity
XX modeling, comprises preparing a gene expression profile of a tissue or
XX cell sample exposed to the compound, and comparing the gene expression
XX profile to a database.
XX
XX Example 4; Page; 446pp; English.
XX
XX The invention relates to a novel method of predicting at least one toxic
XX effect of a compound. The method comprises a gene expression profile of a
XX tissue or cell sample exposed to the compound, and comparing the gene
XX expression profile to a database comprising at least part of the data or
XX information given in the specification. The methods are useful for
XX predicting at least one toxic effect of a compound, predicting the
XX progression of a toxic effect of a compound, predicting the renal
XX toxicity of a compound, or identifying toxicity markers in tissues or
XX cells exposed to known renal toxin. The genes are useful as toxicity
XX markers in drug screening and toxicity assays, in monitoring disease or
XX physiological states, or disease progression. This polynucleotide
XX represents a rat DNA sequence relating to the toxic effect database
XX described in the specification. NOTE: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from the World Intellectual Property
XX Organization
XX
XX Sequence 2065 BP; 435 A; 578 C; 617 G; 435 T; 0 U; 0 Other;
XX
XX Query Match 94.1%; Score 1241.6; DB 10; Length 2065;
XX Best Local Similarity 99.7%; Pred. No. 2.8e-314;
XX Matches 1244; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 73 CTGGAGGTATTGACCGCTAGGCATGATCTACACCGTGGGATCTCATGCTCTCGCC 132
XX |
XX 613 CGGAGGTATTGACCGCTAGGCATGATCTACACCGTGGGATCTCATGCTCTCGCC 672
XX |
XX 133 TCCCTCAGCGTGGCTGCTCATCTCGCTTATTTAGCGGCTGCACTGACCGCAAC 192
XX |
XX 673 TCCCTCAGCGTGGCTGCTCATCTCGCTTATTTAGCGGCTGCACTGACCGCAAC 732
XX |
XX 193 TACATCCACATGCACATGCTCTGCTTTATGCTGCGCGCGGAGCATCTTCTGAAG 252
XX |
XX 733 TACATCCACATGCACATGCTCTGCTTTATGCTGCGCGCGGAGCATCTTCTGAAG 792
XX |
XX 253 GACGCTGCTCTACTCTGGCTTACAGCTGAGCGCGGAGCGCTTACAGAGGAAGAG 312
XX |
XX 793 GACGCTGCTCTACTCTGGCTTACAGCTGAGCGCGGAGCGCTTACAGAGGAAGAG 852
XX |
XX 313 TTGCACATCATCGCGAGGTGCCACCTCCGCGCGGCTGCGCGGTAGGCTACGCTGGC 372
XX |
XX 853 TTGCACATCATCGCGAGGTGCCACCTCCGCGCGGCTGCGCGGTAGGCTACGCTGGC 912
XX |
XX 373 TGCGCGTGGCGGTGACCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 432
XX |
XX 913 TGCGCGTGGCGGTGACCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 972
XX |

Qy 433 GTGGAGGGGCTGTACTTGGCAAGCCTCATCTTCTCATGGCCTTTTCTCAGAGAAGATGAC 492
Db |
Qy 973 GTGGAGGGGCTGTACTTGGCAAGCCTCATCTTCTCATGGCCTTTTCTCAGAGAAGATGAC 1032
Db |
Qy 493 CTGTGGGGCTTCAACCATCTTTGGCTGGGGCTTACCGGCTCTCTTCTGGGGCTGTGGTGC 552
Db |
Qy 1033 CTGTGGGGCTTCAACCATCTTTGGCTGGGGCTTACCGGCTCTCTTCTGGGGCTGTGGTGC 1092
Db |
Qy 553 GGTGTGAGAGCAACCTTTGGCCAAACATCTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 612
Db |
Qy 1093 GGTGTGAGAGCAACCTTTGGCCAAACATCTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 1152
Db |
Qy 613 TGGATCATCAGGTGCGCATCTCTGGGATCTGCTGCTCACTTCACTTCACTCTTTTATCAAC 672
Db |
Qy 1153 TGGATCATCAGGTGCGCATCTCTGGGATCTGCTGCTCACTTCACTTCACTCTTTTATCAAC 1212
Db |
Qy 673 ATCATCCGGGTGCTTGGCACTTAAGCTTCCGGAGACCAATCGGGCGGCTGTGACACAGG 732
Db |
Qy 1213 ATCATCCGGGTGCTTGGCACTTAAGCTTCCGGAGACCAATCGGGCGGCTGTGACACAGG 1272
Db |
Qy 733 CAGCAGTACCGGAAGTGTCTCAGGTCCACGTTGGTGTCTGCTGCGGCTCTTTTGTGTGCAC 792
Db |
Qy 1273 CAGCAGTACCGGAAGTGTCTCAGGTCCACGTTGGTGTCTGCTGCGGCTCTTTTGTGTGCAC 1332
Db |
Qy 793 TACACCGTCTTTCATGGCCTTGGCCTTACACCGAGGTCTCAGGAGCATTTGTGGCAGATCCAG 852
Db |
Qy 1333 TACACCGTCTTTCATGGCCTTGGCCTTACACCGAGGTCTCAGGAGCATTTGTGGCAGATCCAG 1392
Db |
Qy 853 ATGATTTATGAGATGCTCTTCACTCTTCCAGGATTTTGTGGCATTATATCTGT 912
Db |
Qy 1393 ATGATTTATGAGATGCTCTTCACTCTTCCAGGATTTTGTGGCATTATATCTGT 1452
Db |
Qy 913 TTCTGCAATCGTCTGAGGTGAGGAGGATTTAGGAAGTCTAGGAGCGCTCGACACTGGCG 972
Db |
Qy 1453 TTCTGCAATCGTCTGAGGTGAGGAGGATTTAGGAAGTCTAGGAGCGCTCGACACTGGCG 1512
Db |
Qy 973 TTGGACTTCAAGCGCAAGCAACGAAAGTGGAGTAGCAGCTACAGCTATGCGCCCAATGGTG 1032
Db |
Qy 1513 TTGGACTTCAAGCGCAAGCAACGAAAGTGGAGTAGCAGCTACAGCTATGCGCCCAATGGTG 1572
Db |
Qy 1033 TCTCAGCAGTGTGACCATGTTGGGCGCGCTGAGGAGTCTAGGCTTCCCGCTCAGCGCC 1092
Db |
Qy 1573 TCTCAGCAGTGTGACCATGTTGGGCGCGCTGAGGAGTCTAGGCTTCCCGCTCAGCGCC 1632
Db |
Qy 1093 CGCTGCTCTCTGCTTACCAATGGCCTTCCAGCTGCTGCGCATGCGCAAGCCAGG 1152
Db |
Qy 1633 CGCTGCTCTCTGCTTACCAATGGCCTTCCAGCTGCTGCGCATGCGCAAGCCAGG 1692
Db |
Qy 1153 GCTCCAGCCACTGAGACTGAAACCCCTACCACTATGCGCGTTCCTCAAGGACGATGGA 1212
Db |
Qy 1693 GCTCCAGCCACTGAGACTGAAACCCCTACCACTATGCGCGTTCCTCAAGGACGATGGA 1752
Db |
Qy 1213 TTCTTAAAGGCTCTGCTCAGGCTTGGATGAGAGGCTTCCGGGTCTGCGCGCGCCCT 1272
Db |
Qy 1753 TTCTTAAAGGCTCTGCTCAGGCTTGGATGAGAGGCTTCCGGGTCTGCGCGCGCCCT 1812
Db |
Qy 1273 CCATTGTTGAGGAGGATGCGGAAACAGTCTATGCTGCTGGGCACTAGG 1320
Db |
Qy 1813 CCATTGTTGAGGAGGATGCGGAAACAGTCTATGCTGCTGGGCACTAGG 1860
Db |
XX
XX RESULT 7
XX AAQ29606
XX ID AAQ29606 standard; cdna; 2051 BP.
XX
XX AAQ29606;
XX AC
XX XX
XX 25-MAR-2003 (revised)
XX DT 16-MAR-1993 (first entry)
XX XX
XX Rat bone PTH/PTHrP receptor clone, R15B.
XX XX

KW Parathyroid hormone; related protein; calcium; antagonist; antibodies;
KW hypercalcaemia; ss.
XX
OS Rattus rattus.
XX
XX
XX Key Location/Qualifiers
XX CDS 73..1948
XX /*tag= a
XX
XX W09217602-A1.
XX
XX 15-OCT-1992. 92WO-US002821.
XX
XX 06-APR-1992; 92WO-US002821.
XX
XX 05-APR-1991; 91US-00681702.
XX
XX (GEMO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX
XX Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX Schipani E;
XX
XX WPI; 1992-366271/44.
XX P-PSDB; AAR27706.
XX
XX New DNA encoding parathyroid hormone receptor, DNA and antibodies - for
XX (differential) diagnosis of hypercalcaemia, and diagnosis and treatment
XX of tumours.
XX
XX Claim 3; Fig 3; 9lpp; English.
XX
XX Total RNA was isolated from rat osteosarcoma (ROS) cells and used to
XX prep. a cDNA library. The resultant phage libraries were used to
XX transform E. coli contg. a larger helper plasmid p3. The cells were
XX screened to isolate those expressing functionally intact ROS cell
XX parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
XX receptor proteins, performed according to Gearing et al., (EMBO J. 8:
XX 3676, 1989), by identifying colonies capable of binding a suitable
XX radiolabelled ligand. The clone encodes a protein which may be used in a
XX therapeutic compen. to inhibit activation of PTH or PTHrP and thus reduce
XX the level of calcium in the blood. Cops. capable of competing with PTH or
XX PTHrP for binding can be identified using the protein prod. and DNAs
XX homologous to PTH DNA can be identified using fragments of the clone as
XX probes. The sequence may be used for the prodn. of antibodies useful for
XX the treatment, classification, prognosis and/or treatment of disorders
XX related to the interaction between a cell receptor and a ligand such as
XX in hypercalcaemia. See also AAQ29604-11. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX SQ Sequence 2051 BP; 430 A; 576 C; 616 G; 429 T; 0 U; 0 Other;
Query Match 93.9%; Score 1240; DB 2; Length 2051;
Best Local Similarity 99.6%; Pred. No. 5.7e-314;
Matches 1243; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 73 CTGGAGGTATTGACCGCGTAGGCATGATACACCGTGGGATCTCATGTCTCTCGCC 132
DB 613 CGGGAGGTATTGACCGCGTAGGCATGATACACCGTGGGATCTCATGTCTCTCGCC 672
QY 133 TCCCTCAGCGTGGCTGTGCTCATCTCGGCTATTATTAGGCGGCTGCACGCGCAAC 192
DB 673 TCCCTCAGCGTGGCTGTGCTCATCTCGGCTATTATTAGGCGGCTGCACGCGCAAC 732
QY 193 TACATCCACATGCACATGTTCTCTGCTTTATGTCGCGCGCGGAGCATCTTCGTGAAG 252
DB 733 TACATCCACATGCACATGTTCTCTGCTTTATGTCGCGCGCGGAGCATCTTCGTGAAG 792
QY 253 GACGCTGTCTACTCTGGCTTCACGCTGGATGAGCGCGGCGCTCACAGGAAGAG 312
DB 793 GACGCTGTCTACTCTGGCTTCACGCTGGATGAGCGCGGCGCTCACAGGAAGAG 852
QY 313 TTGCACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCCCGGTAGGCTAGCTGGC 372

DB 853 TTGCACATCATCGCGCAGGTGCGCACTCGCGCGCGCTGCGCGCTAGGCTACGCTGGC 912
QY 373 TGCCGCGTGGCGGTGACCTTCTTCTACTTCTGCTGCTACCACTACTACTGATCTCTG 432
DB 913 TGCCGCGTGGCGGTGACCTTCTTCTCTACTTCTGCTGCTACCACTACTACTGATCTG 972
QY 433 GTGGAGGGGCTGTACTTTCACAGCGCTCTTCTCATGCGCTTTTCTTCAGAGAAGAGTAC 492
DB 973 GTGGAGGGGCTGTACTTTCACAGCGCTCTTCTCATGCGCTTTTCTTCAGAGAAGAGTAC 1032
QY 493 CTGTGGGGGCTTACCATCTTTTGGCTGGGGTGTACCGGCTGTCTTCGTGGCTGTGTGGGTC 552
DB 1033 CTGTGGGGGCTTACCATCTTTTGGCTGGGGTGTACCGGCTGTCTTCGTGGCTGTGTGGGTC 1092
QY 553 GGTGTACAGAGCAACCTTTGGCCAAACACTGGGTGCTGGGATCTGAGCTCCGGGCAACAAG 612
DB 1093 GGTGTACAGAGCAACCTTTGGCCAAACACTGGGTGCTGGGATCTGAGCTCCGGGCAACAAG 1152
QY 613 TGGATCATCCAGGTGCCCATCTCTGGGCATCTGTTGTGCTCAACTTCATCTCTTTTATCAAC 672
DB 1153 TGGATCATCCAGGTGCCCATCTCTGGGCATCTGTTGTGCTCAACTTCATCTCTTTTATCAAC 1212
QY 673 ATCATCCGGGTGCTTGCCTAAGCTTCCGGAGACCAATGCGGGCGGGTGTGACACAGG 732
DB 1213 ATCATCCGGGTGCTTGCCTAAGCTTCCGGAGACCAATGCGGGCGGGTGTGACACAGG 1272
QY 733 CAGCAGTACCGGAAGCTGCTCAGGTCCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 792
DB 1273 CAGCAGTACCGGAAGCTGCTCAGGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1332
QY 793 TACACGCTCTTCATGCGCTTTCGCGTACACCGAGGTCTCAGGGACATTTGTGGCAGATCCAG 852
DB 1333 TACACGCTCTTCATGCGCTTTCGCGTACACCGAGGTCTCAGGGACATTTGTGGCAGATCCAG 1392
QY 853 ATGCATTATGAGATGCTCTTCAACTCCAGCGAGGATTTTGTGGTGCATCATATACTGT 912
DB 1393 ATGCATTATGAGATGCTCTTCAACTCCAGCGAGGATTTTGTGGTGCATCATATACTGT 1452
QY 913 TTCTGCAATGGTGTGAGGTGCGGAGATTTAGGAAGTTCATGGAGCGGCTGGACACTGGCG 972
DB 1453 TTCTGCAATGGTGTGAGGTGCGGAGATTTAGGAAGTTCATGGAGCGGCTGGACACTGGCG 1512
QY 973 TTGCACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATATGGCCCAATGGTG 1032
DB 1513 TTGCACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATATGGCCCAATGGTG 1572
QY 1033 TCTCACAAGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCTTCCCTTCAGCCCC 1092
DB 1573 TCTCACAAGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCTTCCCTTCAGCCCC 1632
QY 1093 CGCTGCTCTCTGCGCACTACCAATGGCCACTCCAGCTGCGCTGGCCATGCCAAGCCAGGG 1152
DB 1633 CGCTGCTCTCTGCGCACTACCAATGGCCACTCCAGCTGCGCTGGCCATGCCAAGCCAGGG 1692
QY 1153 GCTCCAGCCACTCAGACTGAAACCCCTACAGTCACTATATGGCGGTTCCCAAGAGCAGTGA 1212
DB 1693 GCTCCAGCCACTCAGACTGAAACCCCTACAGTCACTATATGGCGGTTCCCAAGAGCAGTGA 1752
QY 1213 TTCTTTAAACGGCTCTCTGCTCAGGCTTGGATGAGGAGGCTTCCGGGTGTGCGCGCGCCT 1272
DB 1753 TTCTTTAAACGGCTCTCTGCTCAGGCTTGGATGAGGAGGCTTCCGGGTGTGCGCGCGCCT 1812
QY 1273 CCATTGTTGAGGAAGATGGGAAACAGTCACTGTGACTGGGCACTAGG 1320
DB 1813 CCATTGTTGAGGAAGATGGGAAACAGTCACTGTGACTGGGCACTAGG 1860
RESULT 8
ADO30323 standard; cDNA; 1776 BP.
ID ADO30323
XX AC ADO30323;
XX AC ADO30323;

DT	29-JUL-2004 (first entry)	
XX	Mouse GPCR PTHR1 polynucleotide, SEQ ID NO:1426.	
DE	G protein-coupled receptor; GPCR; drug screening; diagnosis;	
XX	transgenic mouse; neurological disorder; adrenal gland disorder;	
KW	colon disorder; intestinal disorder; cardiovascular disorder;	
KW	muscular disorder; blood disorder; immune disorder; bone disorder;	
KW	joint disorder; metabolic disorder; nutritive disorder; cancer;	
KW	kidney disorder; liver disorder; lung disorder; breast disorder;	
KW	ovary disorder; uterus disorder; prostate disorder; testis disorder;	
KW	skin disorder; stomach disorder; pancreas disorder; spleen disorder;	
KW	thyroid disorder; thyroid disorder; antiparkinsonian; antimanic;	
KW	cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;	
KW	CNS; central nervous system; respiratory; antiarrhythmic; antidiabetic;	
KW	virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;	
KW	dermatological; antitumor; antithyroid; antiallergic; anorectic;	
KW	immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;	
KW	murine; gene; ss.	
XX	Mus musculus.	
OS	WO2004040000-A2.	
XX	13-MAY-2004.	
XX	09-SEP-2003; 2003WO-US028226.	
XX	09-SEP-2002; 2002US-0409303P.	
XX	09-APR-2003; 2003US-0461329P.	
XX	(PRIM-) PRIMAL INC.	
PA	Gaitanaris GA, Bergmann JB, Gragerov A, Hohmann J, Li F;	
XX	Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;	
PI	WPI; 2004-390329/36.	
DR	P-PSDB; ADO29629.	
XX	Novel mammalian G protein coupled receptors, useful for identifying	
PT	compounds that modulates diagnosing and treating disease condition	
PT	associated with GPCR dysfunction e.g. autoimmune diseases, angina	
PT	pectoris, Parkinson's disease.	
XX	Claim 151; SEQ ID NO 1426; 542pp; English.	
PS	The invention relates to human and mouse G protein-coupled receptors	
XX	(GPCRs) and nucleic acids encoding them. The invention also relates to	
CC	sequences at least 90% identical to the GPCR proteins and nucleic acids	
CC	of the invention; methods of treating, preventing or diagnosing diseases	
CC	associated with GPCRs of the invention; methods of screening for	
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	
CC	from the transgenic mice; kits comprising several mice, each of which has	
CC	a mutation in a different GPCR gene of the invention; and kits comprising	
CC	probes which hybridize to GPCR polynucleotides of the invention. The	
CC	invention further discloses variants of the GPCR polypeptides and vectors	
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	
CC	be used in the diagnosis, treatment or prevention of a wide variety of	
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	
CC	disorders of the adrenal gland; disorders of the colon or intestine	
CC	(e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel	
CC	syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or	
CC	myocardial infarction); muscular disorders; blood disorders (e.g.,	
CC	anemia or leukaemia); immune disorders (e.g., autoimmune disorders or	
CC	AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid	
CC	arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,	
CC	obesity, enzyme deficiency-related diseases or vitamin deficiency-related	
CC	diseases); and disorders of the kidney, liver, lung, breast, ovary,	
CC	uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and	
CC	thyroid (e.g., cancers). The present sequence represents a GPCR-encoding	

CC nucleic acid of the invention. Note: The full sequence data for this
patent did not form part of the printed specification; those sequences
not shown were obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

CC	Sequence 1776 BP; 364 A; 519 C; 500 G; 393 T; 0 U; 0 Other;	
XX	Query Match	86.8%; Score 1146.4; DB 12; Length 1776;
SQ	Best Local Similarity	95.5%; Pred. No. 1.6e-289;
	Matches 1180; Conservative	0; Mismatches 56; Indels 0; Gaps 0;
Qy	73	CTGGAGGATTTTACCCGCTAGGCATCATCTACACCGTGGGATATCCATGCTCTCTCGCC 132
Db	541	CGGAGGATTTTACCCGCTAGGCATCATCTACACCGTGGGATATTCATGCTCTCTCGCC 600
Qy	133	TCCCTCACCGTGGCTGCTGCATCTCCGCTATTTTAGGCGGCTGCATGCACCGCAAC 192
Db	601	TCCCTCACCGTGGCTGCTGCATCTCCGCTATTTTAGGCGGCTGCATGCACCGCAAC 660
Qy	193	TATATCCATGACATGTTCTCTGTTATGTCGCGCGCGGAGCATCTTCGTGAAG 252
Db	661	TATATCCATGACATGTTCTCTGTTATGTCGCGCGCGGAGCATCTTCGTGAAG 720
Qy	253	GACGCTGTGCTTACTCTGCTTACGCTGGATGAGCGCGCTCACAGAGAGAG 312
Db	721	GACGCTGTGCTTACTCTGCTTACGCTGGATGAGCGCGCTCACAGAGAGAG 780
Qy	313	TTGCATCATTCGCGAGGTGCCACCTCCGCGCGCTCCGCGCGCTCCGCGCGCTGGC 372
Db	781	TTGCATCATTCGCGAGGTGCCACCTCCGCGCGCTCCGCGCGCTCCGCGCGCTGGC 840
Qy	373	TGCGCGTGGCGTGACCTTTCTCTACTTCTTGCTTACCACTACTACTGATCTG 432
Db	841	TGCGCGTGGCGTGACCTTTCTCTACTTCTTGCTTACCACTACTACTGATCTG 900
Qy	433	GTGAGGGGCTGTACTTGCACAGCTCTTATGCGGCTTTTCTCAGAGAGAGTAC 492
Db	901	GTGAGGGGCTGTACTTGCACAGCTCTTATGCGGCTTTTCTCAGAGAGAGTAT 960
Qy	493	CTGTGGGGCTTACCACTTTGCTGGGGCTTACCGGCTCTCTTCTGGTGGTGGTGC 552
Db	961	CTGTGGGGCTTACCACTTTGCTGGGGCTTACCGGCTCTCTTCTGGTGGTGGTGC 1020
Qy	553	GGTGTGAGAGCAACCTTTGGCCAACTGTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 612
Db	1021	GGTGTGAGAGCAACCTTTGGCCAACTGTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 1080
Qy	613	TGATCATTCAGGTGGCCATCTTGGCATCTGTTGCTCAACTTCATCTTTTATCAAC 672
Db	1081	TGATCATTCAGGTGGCCATCTTGGCATCTGTTGCTCAACTTCATCTTTTATCAAC 1140
Qy	673	ATCATCGGGTGTGCTGCTCACTTAAGCTTTCGGGAGCAATTCGGGCGGCTGACACCAAG 732
Db	1141	ATCATCGGGTGTGCTGCTCACTTAAGCTTTCGGGAGCAATTCGGGCGGCTGACACCAAG 1200
Qy	733	CAGCAGTACCGGAAGTGTCTCAGGTCCACGCTTGGTGTCTGCTGGCTCTTTTGTGTGCAC 792
Db	1201	CAGCAGTACCGGAAGTGTCTCAGGTCCACGCTTGGTGTCTGCTGGCTCTTTTGTGTGCAC 1260
Qy	793	TACACGCTTTTACGCGCTTTCGCTACACCGAGGTCTCAGGAGCATTTGTGGAGATCCAG 852
Db	1261	TACACGCTTTTACGCGCTTTCGCTACACCGAGGTCTCAGGAGCATTTGTGGAGATCCAG 1320
Qy	853	ATCATTTATGAGATGCTCTTCACTCTTCCAGGATTTTCTTGCATCATATATCTGT 912
Db	1321	ATCATTTATGAGATGCTCTTCACTCTTCCAGGATTTTCTTGCATCATATATCTGT 1380
Qy	913	TTCTGCAATGGTGGTGGAGGATTTAGGAAGTTCATGGAGCGCTGGACACTGGCG 972
Db	1381	TTCTGCAATGGTGGTGGAGGATTTAGGAAGTTCATGGAGCGCTGGACACTGGCA 1440
Qy	973	TTGGATTTCAAGCGCAAGACCAAGATGGAGGTAGAGCTTACAGCTATGGCCCAATGGTG 1032

Db 601 CTGCCAACACCGGGTCTGGGACTTCGAGCTCCGGGAACAAAAGTGGATCATCCAGGTG 660
Qy 628 CCATCTCGGCACTGTGTGCTCAACTTCATCTCTTTTATCAACATCATCCGGTGTCTT 687
Db 661 CCATCTCGGCTCCATTTGTCTCAACTTCATCTCTTTTATCAACATCATCCGGTGTCTC 720
Qy 688 GCCACTAAGCTTCGGGAGACCAATGCGGGCGGTGTGACACCCAGGAGCGAGTACCGGAAG 747
Db 721 GCCACCAAGCTGCGGGAGACCAACGCCGGCGGTGTGACACACCGCAGCAGTACCGGAAG 780
Qy 748 CTGCTCAGGTCACAGTGTGTGTGCTCGTCCGCTCTTTTGTGTGCACTACACCGTCTTCATG 807
Db 781 CTGCTCAATCCAGCTGTGTGCTCATGCCCTCTTTGGCGTCCACTACATTTGTTTCATG 840
Qy 808 GCCTTGGCGGTACACCGAGTCTCAGGACATTTAGGACATTTGGGAGATCCAGATGCAATTTAGATG 867
Db 841 GCCACACATACACCGAGGTCTCAGGAGCGCTCTGGCAAGTCCAGATGCACTATGAGATG 900
Qy 868 CTCTTCAACTCTTCCAGGGAATTTTGTGCAATCATATCTGTTTCTGCAATGGTGAG 927
Db 901 CTCTTCAACTCTTCCAGGGAATTTTGTGCAATCATATCTGTTTCTGCAATGGTGAG 960
Qy 928 GTGCAGGACAGATTTAGGAACTCATGAGCGCGCTGGACACTGGCGTTGGACTTCAAGCGC 987
Db 961 GTACAAGCTGAGATCAAGAAATCTTGGAGCGCTGGACACTGGCACTGGACTTCAAGCGA 1020
Qy 988 AAGCAGCAAGTGGGAGTAGCAGTACAGTATATGGCCCAATGTGTCTCTCACAGAGTGTG 1047
Db 1021 AAGCAGCGCAGCGGAGCAGCAGTATAGTACGCGCCCATGTGTGTCCACACAAAGTGTG 1080
Qy 1048 ACCAATGTGGCCCCCGTGCAGGACTCAGCTCCCTCCCTCAGCCCCGCG---CTGCTCTCT 1104
Db 1081 ACCAATGTGGCCCCCGTGTGGGACTCGGCTCGCTCCCTCAGCCCCGCGCTACTGCCCACT 1140
Qy 1105 GCCACTACCAATGGCCACTCCAGCTGCTGGCCATGCCAAGCAGGCGGTCCAGCCACT 1164
Db 1141 GCCACCAACGAGCCACCTCAGCTGCCTGGCCATGCCAAGCAGGAGCCCCAGCCCTG 1200
Qy 1165 GAGAC---TGAAACCTTACAGTCACTATGGCGGTTCCTCAAGGACGATGGATTCCTTAAC 1221
Db 1201 GAGACCTTCGAGACACACCACTTGCCTGCTCTCCCAAGGACGATGGGTTCCTCAAC 1260
Qy 1222 GGCTCTGCTCAGGCTTGGATGAGGAGCGCTTCGGGCTGCGGCGCGCTCCATTGTG 1281
Db 1261 GGCTCTGCTCAGGCTTGGAGGAGCGCTTCTGGGCTGAGCGGCGCACCTGCGCTCTA 1320
Qy 1282 CAGGAAGGATGGGAAACAGTCACTGTGACTGGGCACTAGG 1320
Db 1321 CAGGAAGTGGGAGACAGTCACTGTGACCAGGCGCTGG 1359

RESULT 11
AAA51737
ID AAA51737 standard; DNA; 1380 BP.
XX AC AAA51737;
XX 31-OCT-2000 (first entry)
XX Human tethered PTH-1 receptor, Tether-R11, coding sequence.
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FT 1..1353
CDS /*tag= a
/product= "Tether-R11"

PN WO200039278-A2.
XX 06-JUL-2000.
PF 30-DEC-1999; 99WO-US031108.
XX 31-DEC-1998; 98US-0114577P.
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
DR P-PSDB; AAY96988.
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
FT treating mammalian conditions characterized by decreases in bone mass.
XX Example 4; Fig 19; 119pp; English.
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX SQ Sequence 1380 BP; 245 A; 461 C; 388 G; 286 T; 0 U; 0 Other;
Query Match 74.2%; Score 979.4; DB 3; Length 1380;
Best Local Similarity 84.5%; Pred. No. 7.4e-246;
Matches 1154; Conservative 0; Mismatches 166; Indels 45; Gaps 3;
Qy 1 ATGGGGCGCGCCCGGATGCGACCCAGCTGGCGCTCTCTACTCTGCTGCCAGTGTCTCAGC 60
Db 1 ATGGGGACCGCCCGGATGCGACCCCGCTGGCGCTCTCTCTGCTGCCCGCTCTCAGC 60
Qy 61 TCCGCAATATGCGCTG-----GAGGTA 81
Db 61 TCCGCGTACCGGTTCGCGAATCCAGTATGATGATGCGTGGCGGAGGCGGAGGTG 120
Qy 82 TTTGACCGCTTAGGCATGATCTACCGTGGGATCTCCATGTCCTCTCGCTCCCTCAGC 141
Db 121 TTTGACCGCTTGGCGATGATTTACACGCTGGGTACTCCGCTGCTCCCTCAGC 180
Qy 142 GTGGCTGTGCTCATCTCTGGCTATTTTAGCGGCTGCACTGACGCGCACTACATCCAC 201
Db 181 GTAGCTGTGCTCATCTCTGGCTACTTTTAGCGGCTGCACTGACGCGCACTACATCCAC 240
Qy 202 ATCCACATGTTCTCTGCTGTTTATGCTGCGCGCGCGAGCATCTTCTGTAAGGACGCTGTG 261
Db 241 ATGACCTGTTCTCTGCTCTCTGCTGCTGCGCGCGTGTGAGCATCTTCTGTAAGGACGCTGTG 300
Qy 262 CTCTACTCTGGCTTACGCTTGGATGAGCGCGCGCTCTCACAGAGGAAGATTGCAATC 321
Db 301 CTCTACTCTGGCGCCACCGCTTGTATGAGGCTGAGCGCTCACCGGAGGAGCTGGCGCC 360
Qy 322 ATCGCGGAGTGCACCTCGCGCGCGCTGCGCGGTAGGCTAGCTGCTGCGCGGTG 381
Db 361 ATCGCGGAGCGCGCGCGCTGCGCGCTGCGCGGTAGCTGCTGCGCGGTGCGGAGGTG 420

Db 181 TGACGGCGCACTACATCCATGCAATGTTCTGCTGTTATGTCGCGCGCGGAGC 240
Qy 241 ATCTTCGTGAAGACGCTGCTCTACTCTGGCTTCACTGATGAGCGCGCGCTC 300
Db 241 ATCTTCGTGAAGACGCTGCTCTACTCTGGCTTCACTGATGAGCGCGCGCTC 300
Qy 301 ACAGAGAAAGTTGACATCATCGCGAGGTGCGGCGCTGCGCGCGGTA 360
Db 301 ACAGAGAAAGTTGACATCATCGCGAGGTGCGGCGCTGCGCGCGGTA 360
Qy 361 GGCTACGCTGGCTGCGCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 420
Db 361 GGCTACGCTGGCTGCGCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 420
Qy 421 TACTGGATCTGTTGGAGGGGTGTTACTTGACAGCGCTCATCTTCATGCGCTTTCATCA 480
Db 421 TACTGGATCTGTTGGAGGGGTGTTACTTGACAGCGCTCATCTTCATGCGCTTTCATCA 480
Qy 481 GAGNAGAGTACCTGTTGGGCTTCAACCATCTTTGGCTGGGCTTACCGGCTGTTGCTG 540
Db 481 GAGNAGAGTACCTGTTGGGCTTCAACCATCTTTGGCTGGGCTTACCGGCTGTTGCTG 540
Qy 541 GCTGTGTTGGTTCGCTGTCAGAGCAACCTTGCCAACTGCGGCTGCGGATCTGAGCTCC 600
Db 541 GCTGTGTTGGTTCGCTGTCAGAGCAACCTTGCCAACTGCGGCTGCGGATCTGAGCTCC 600
Qy 601 GGGCACAAGAGTGGATCATCCAGGTGCCATCTGGCATCTGTGTGCTCAACTTCATC 660
Db 601 GGGCACAAGAGTGGATCATCCAGGTGCCATCTGGCATCTGTGTGCTCAACTTCATC 660
Qy 661 CTTTTATCAACATCATCCGGTCTGCGCACTAAGCTTCGGGAGACCAATGCGGCGCG 720
Db 661 CTTTTATCAACATCATCCGGTCTGCGCACTAAGCTTCGGGAGACCAATGCGGCGCG 720
Qy 721 TGTGACACCGGAGGAGTACCGGAAGCTGCTCAGGTCCACGTTGCTGCTGCGGCTC 780
Db 721 TGTGACACCGGAGGAGTACCGGAAGCTGCTCAGGTCCACGTTGCTGCTGCGGCTC 780
Qy 781 TTTGGTGTGCACTACACCGCTTTCATGCGCTTTCGCGTACACCGAGTCTCAGGACATTG 840
Db 781 TTTGGTGTGCACTACACCGCTTTCATGCGCTTTCGCGTACACCGAGTCTCAGGACATTG 840
Qy 841 TGGCAGATCCAGATGCAATGATGATGCTCTTCACTCTTCAGGATTTTGTGTC 900
Db 841 TGGCAGATCCAGATGCAATGATGATGCTCTTCACTCTTCAGGATTTTGTGTC 900
Qy 901 ATCATATCTGTTTCTGCAATGAGGTGAGGTGAGGAGATGAGAAATGATGAGGCGCG 960
Db 901 ATCATATCTGTTTCTGCAATGAGGTGAGGTGAGGAGATGAGAAATGATGAGGCGCG 960
Qy 961 TGGACACTGGCGTTG 975
Db 961 TGGACACTGGCGTAG 975

RESULT 13
ABZ42719
ID ABZ42719 standard; DNA; 1948 BP.
XX AC ABZ42719;
XX AC ABZ42719;
XX DT 04-MAR-2003 (first entry)
XX DE Human parathyroid hormone receptor 1 nucleotide SEQ ID NO:228.
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer; gene; ds.
XX Homo sapiens.
XX WO200261087-A2.
XX 08-AUG-2002.
XX 19-DEC-2001; 2001WO-US050107.
XX 19-DEC-2000; 2000US-0257144P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
XX P-PSDB; ABP81872.
XX New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.
XX Disclosure; Fig 1; 523pp; English.
XX The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 13-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
XX SQ Sequence 1948 BP; 405 A; 600 C; 570 G; 373 T; 0 U; 0 Other;

Query Match 73.2%; Score 966.8; DB 8; Length 1948;
Best Local Similarity 86.6%; Pred. No. 1.7e-242;
Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;
Qy 69 TGGCGCTGGAGGTATTTGACCGCTAGGCATGATCTACCGTGGGATCTCCATGTCTCT 128
Db 565 TGAACGGAGGTGTTTACCGCTGGCATGATTTACCGTGGGCTGCACTGTCCT 624
Qy 129 CGGCTCCCTCACGGTGGCTGTGCTCATCTCGGCTATTTTAGCGGCTGCACGCG 188
Db 625 GGGTCCCTCACCGTAGTGTGCTCATCTCGGCTACTTTTAGCGGCTGCACTGCGCG 684
Qy 189 CAATCATCATCCATGACATGTTCTGCTGTTATGCTGCGCGCGCGAGCATCTTCGT 248
Db 685 CAATCATCATCCATGACCTGTTCTGCTGTTCTTCATGCTGCGCGCGGTGAGCATCTTCGT 744


```
Qy 189 CAACTACATCCACATGTTCTCGTTCCTGCTGCGCGCGGAGCAGTCTTCGT 248
Db 685 CAACTACATCCACATGTTCTCGTTCCTGCTGCGCGCGGAGCAGTCTTCGT 744
Qy 249 GAAGGACGCTGTGCTCTACTCTGCTTTACGCTTGATGAGCGCGAGCCTTCACAGGGA 308
Db 745 CAAGGACGCTGTGCTCTACTCTGCGCCACGCTGTGATGAGGCTGAGCGCTCACCGAGGA 804
Qy 309 AGAGTTGCATCATGTCGGGAGTGCCACCTCGCGCGCGCGCTGCGCGCTAGGCTACGC 368
Db 805 GGAGCTCGCGGCTTACCGCCAGCGCGCGCGCGCTGCGCGCGCTGCGCGCTACGC 864
Qy 369 TGCTGCGCGGTGCGGTGACCTTCTTCTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCT 428
Db 865 GGGCTGAGGGTGCTGTGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 924
Qy 429 CTTGTTGAGGGGCTGTACTTTGACAGCGCTCATCTTTCATGCGCTTTTCTTCTTCTTCTT 488
Db 925 TCTGTTGAGGGGCTGTACTTTGACAGCGCTCATCTTTCATGCGCTTTCTTCTTCTTCTTCT 984
Qy 489 GTACTGTGGGGCTTACCAATCTTTTGGCTGGGTCTTACCGGCTGTCTTCTGCTGTGTGTG 548
Db 985 GTACTGTGGGGCTTACCAATCTTTTGGCTGGGTCTTACCGGCTGTCTTCTGCTGTGTGTG 1044
Qy 549 GGTGCGGTGTCAGAGCAACCTTTGGCAACACTGGGTGCTGGGATCTGAGCTCCGGGACAA 608
Db 1045 GGTGAGTGTGAGAGTACCTTGGCAACACTGGGTGCTGGGATCTGAGCTCCGGGACAA 1104
Qy 609 GAAGTGGATCATCCAGGTGCCATCTCTGGCATCTGTTGTCTCAACTTCTTCTTTTAT 668
Db 1105 AAGTGGATCATCCAGGTGCCATCTCTGGCATCTGTTGTCTCAACTTCTTCTTTAT 1164
Qy 669 CAACATCATCGGGTGTGCTTGCATTAAGCTTGGGAGACCAATGCGGGCGGCTGTGACAC 728
Db 1165 CAATATCTCGGGTGTGCTTGCATTAAGCTTGGGAGACCAATGCGGGCGGCTGTGACAC 1224
Qy 729 CAGCAGCAGTACCGGAGTGTCTCAGGTTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 788
Db 1225 ACGCAGCAGTACCGGAGTGTCTCAGGTTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1284
Qy 789 GCACTACACGCTTTCATGCGCTTTCGCGTACCGAGGTCTCAGGGACATTTGTGGCAGAT 848
Db 1285 CCATCATATTGCTTTCATGCGCACACCATACCGAGGTCTCAGGGACGCTTGGCAAGT 1344
Qy 849 CCAGATGCATATGAGATGCTTTCATCTCTTCCAGGATTTTGTTCGCATCATATA 908
Db 1345 CCAGATGCATATGAGATGCTTTCATCTCTTCCAGGATTTTGTTCGCATCATATA 1404
Qy 909 CTGTTTCTGCAATGCTCAGGTGACGAGCAGAGATTAGGAAGTCTAGGAGCGCTGGACCT 968
Db 1405 CTGTTTCTGCAATGCTCAGGTGACGAGCAGAGATTAGGAAGTCTAGGAGCGCTGGACCT 1464
Qy 969 GGGCTTTGGACTTCAAGCGCAAGCAGCAAGTGGGAGTGGAGCTACAGCTATGCGCCAAAT 1028
Db 1465 GGCACCTGACTTCAAGCGCAAGCAGCAGCGGAGCAGCAGCTATAGTACGCGCCCAT 1524
Qy 1029 GGTGCTCTACAGAGTGTGACCAATGTGGGCGCCCGCTGCGAGGACTCAGCTCCCGCTCAG 1088
Db 1525 GGTGCTCTACAGAGTGTGACCAATGTGGGCGCCCGCTGCGAGGACTCAGCTCCCGCTCAG 1584
Qy 1089 CCCCCGCTCTGCTGCTACCAATGCGCACTCCAGCTGCTGCGGATGCGGATGCGCA 1145
Db 1585 CCCCCGCTCTGCTGCTACCAATGCGCACTCCAGCTGCTGCGGATGCGGATGCGCA 1644
Qy 1146 GCCAGGGGCTCCAGGCACTGAGAC---TGAAACCTTACCAAGTCACTATGCGGTTCCAA 1202
Db 1645 GCCAGGGGCTCCAGGCACTGAGAC---TGAAACCTTACCAAGTCACTATGCGGTTCCAA 1704
Qy 1203 GGACGATGGATTCTTAAAGGCTCTGCTCAGGCTGGATGAGGAGGCTCCGGGTCTGC 1262
Db 1705 GGACGATGGATTCTTAAAGGCTCTGCTCAGGCTGGATGAGGAGGCTCCGGGTCTGC 1764
Qy 1263 GCGGCGGCTTCTTGTGAGGAAGGATGGMAACAGTCACTGTGACTGGGCACTAGG 1320
```

```
Db 1765 GCGGCCACCTGCTCTACAGGAGCTGGGAGACAGTCACTGTGACCGCGCTGGG 1822
```

RESULT 15

```
ADL13887
ID ADL13887 standard; DNA; 1948 BP.
```

```
XX ADL13887;
```

```
XX DT 06-MAY-2004 (first entry)
```

```
XX Osteoarthritis-associated polymorphic nucleotide #419.
```

```
XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
```

```
XX Joint space narrowing; osteophyte development; joint pain;
```

```
XX osteoarthritis; SNP; single nucleotide polymorphism.
```

```
XX Homo sapiens.
```

```
XX WO2003054166-A2.
```

```
XX PD 03-JUL-2003.
```

```
XX PF 19-DEC-2002; 2002WO-US041225.
```

```
XX XX 20-DEC-2001; 2001US-0342603P.
```

```
XX (INCY-) INCYTE GENOMICS INC.
```

```
XX Jones KA, Schafer A;
```

```
XX WPI; 2003-559141/52.
```

Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polynucleotide encoding a protein.

Disclosure; SEQ ID NO 419; 297pp; English.

The invention relates to a method of determining susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain comprising identifying whether the individual has at least one polymorphism in a polynucleotide encoding at least one of the protein listed in the specification. The methods, composition and agent are useful for modulating the susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain that is associated with a disease, preferably osteoarthritis. The cell line and the non-human animal are useful for screening for an agent for diagnosing an individual having susceptibility to joint space narrowing and/or osteophyte development and/or joint pain. This sequence corresponds to the polynucleotide encoding a protein listed in the specification. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).

Sequence 1948 BP; 405 A; 601 C; 569 G; 373 T; 0 U; 0 Other;

Query Match 73.2%; Score 966.8; DB 10; Length 1948;

Best Local Similarity 86.6%; Pred. No. 1.7e-242;

Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

```
Qy 69 TGGCTGGAGGTATTTGACCGCTAGCATGATCTACACGCTGGGATCTCCATGCTCT 128
```

```
Db 565 TGAACGGGAGGTGTTTGACCGCTGGGATGATTTACCGTGGGCTACTCCGTGCCCT 624
```

```
Qy 129 CGCTCCCTCACGCTGCTGCTCATCTGGCTATTTTAGCGGCTGCACCTGCACGCG 188
```

```
Db 625 GGGCTCCCTCACCGTAGTGTGCTCATCTGGCTACTTTAGCGGCTGCACCTGCACGCG 684
```

```
Qy 189 CAACTACATCCACATGTTCTCGTTCCTGCTGCGCGCGGAGCAGTCTTCGT 248
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 23:49:33 ; Search time 254 Seconds
(without alignments)
8503.485 Million cell updates/sec

Title: US-09-869-565-1

Perfect score: 1320

Sequence: 1 atggggcccgccggatgcg.....tcattgtactgggcaactagg 1320

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1243.2	94.2	2051	1	US-07-864-475A-3
2	1243.2	94.2	2051	2	US-08-468-249A-3
3	966.8	73.2	1948	4	US-09-016-434-1253
4	965.2	73.1	2010	1	US-07-864-475A-4
5	965.2	73.1	2010	2	US-08-468-249A-4
6	959.6	72.7	1782	4	US-09-826-509-562
7	931.6	52.4	1863	1	US-07-864-475A-2
8	691.6	52.4	1863	2	US-08-468-249A-2
9	681.2	51.6	1862	1	US-07-864-475A-1
10	681.2	51.6	1862	2	US-08-468-249A-1
11	554.6	42.0	1609	4	US-09-449-632-1
12	387.4	29.3	2003	3	US-08-468-011A-1
13	387.4	29.3	2003	3	US-09-236-468A-1
14	387.4	29.3	2003	5	PCT-US95-07085-1
15	387.4	29.3	2152	4	US-09-449-632-3
16	387.4	29.3	2641	4	US-09-016-434-1463
17	385.8	29.2	1653	4	US-09-826-509-564
18	196.6	14.9	1377	1	US-08-112-817C-1
19	192.4	14.6	1374	4	US-09-826-509-578
20	177.8	13.5	2025	4	US-09-016-434-1063
21	176.2	13.3	1401	4	US-09-826-509-506
22	175.4	13.3	1578	4	US-09-016-434-1377
23	175.4	13.3	1809	1	US-08-453-956-24
24	175.4	13.3	1809	1	US-08-086-631-24
25	175.4	13.3	1809	2	US-08-452-930-24
26	175.4	13.3	1809	5	PCT-US93-08174-24
27	172.8	13.1	1323	4	US-09-826-509-566

28 172.8 13.1 1616 4 US-09-016-434-1451 Sequence 1451, Ap
29 169.4 12.8 2616 4 US-09-016-434-1358 Sequence 1358, Ap
30 168.4 12.8 3066 1 US-08-142-439A-1 Sequence 1, Appli
31 168.4 12.8 3066 2 US-08-869-477-1 Sequence 1, Appli
32 166.2 12.6 1455 2 US-08-811-897A-31 Sequence 31, Appl
33 166.2 12.6 1455 2 US-08-855-213-31 Sequence 31, Appl
34 166.2 12.6 1455 3 US-09-201-474-31 Sequence 31, Appl
35 166.2 12.6 2730 2 US-08-811-897A-39 Sequence 39, Appl
36 166.2 12.6 2730 2 US-08-855-213-39 Sequence 39, Appl
37 166.2 12.6 2730 3 US-09-201-474-39 Sequence 39, Appl
38 158.8 12.0 1875 1 US-08-453-956-14 Sequence 14, Appl
39 158.8 12.0 1875 1 US-08-086-631-14 Sequence 14, Appl
40 158.8 12.0 1875 2 US-08-452-930-14 Sequence 14, Appl
41 158.8 12.0 1875 5 PCT-US93-08174-14 Sequence 14, Appl
42 151.4 11.5 1401 2 US-08-811-897A-32 Sequence 32, Appl
43 151.4 11.5 1401 2 US-08-855-213-32 Sequence 32, Appl
44 151.4 11.5 1401 3 US-09-201-474-32 Sequence 32, Appl
45 151.4 11.5 1869 2 US-08-811-897A-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-07-864-475A-3
; Sequence 3, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; TITLE OF INVENTION: AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2051
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-07-864-475A-3

Query Match

94.2%; Score 1243.2; DB 1; Length 2051;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 73 CTGAGGATTTTACCGCCTAGGATGATCTACACGCTGGGATATCTCAATGTCCTCGCC 132
Db |
Db 613 CGGAGGATTTTACCGCCTAGGATGATCTACACGCTGGGATATCTCAATGTCCTCGCC 672
Qy 133 TCCCTCAGGCTGGCTGCTCATCTCGCCCTATTTTAGGGGCTGCACTGCACGCGCAAC 192
Db |
Db 673 TCCCTCAGGCTGGCTGCTCATCTCGCCCTATTTTAGGGGCTGCACTGCACGCGCAAC 732
Qy 193 TACATCACATGACATGTTCTCTGCTTATGCTGCGCGCGGAGCATCTTCTGTAAG 252
Db |
Db 733 TACATCACATGACATGTTCTCTGCTTATGCTGCGCGCGGAGCATCTTCTGTAAG 792
Qy 253 GACGCTGCTCTACTCTGGCTTCACTGATGAGCGCGGAGCATCTGCAAGAGAAAG 312
Db |
Db 793 GACGCTGCTCTACTCTGGCTTCACTGATGAGCGCGGAGCATCTGCAAGAGAAAG 852
Qy 313 TTGCACATCATCGCGAGGTGCACTCCGCGCGCGCTGCGCGCTAGGCTAGGCTGCG 372
Db |
Db 853 TTGCACATCATCGCGAGGTGCACTCCGCGCGCGCTGCGCGCTAGGCTAGGCTGCG 912
Qy 373 TGCGCGTGGGGTGACCTTCTCTCTACTTCTGCTACCACTACTACTGATCCTG 432
Db |
Db 913 TGCGCGTGGGGTGACCTTCTCTCTACTTCTGCTACCACTACTACTGATCCTG 972
Qy 433 GTGAGGGGCTGTAATTTGACAGCCTCATCTTTCATGCGCTTTTCTCAGAGAAATAC 492
Db |
Db 973 GTGAGGGGCTGTAATTTGACAGCCTCATCTTTCATGCGCTTTTCTCAGAGAAATAC 1032
Qy 493 CTGTGGGGCTTACACATCTTGGCTGGGCTTACGGCTGCTTCTGCTGGCTGCTGG 552
Db |
Db 1033 CTGTGGGGCTTACACATCTTGGCTGGGCTTACGGCTGCTTCTGCTGGCTGCTGG 1092
Qy 553 GGTGTACAGCAACCTTGGCCAACTGGGCTGGGATCTGAGCTCGGGGCAAGAAAG 612
Db |
Db 1093 GGTGTACAGCAACCTTGGCCAACTGGGCTGGGATCTGAGCTCGGGGCAAGAAAG 1152
Qy 613 TGGATCATCCAGGTGCGCATCTGTTGCTGCTCAACTTTTATCAAC 672
Db |
Db 1153 TGGATCATCCAGGTGCGCATCTGTTGCTGCTCAACTTTTATCAAC 1212
Qy 673 ATCATCCGGGTGCTGCACTAAGCTCGGAGACCAATCGGCGCGGTGACACAGG 732
Db |
Db 1213 ATCATCCGGGTGCTGCACTAAGCTCGGAGACCAATCGGCGCGGTGACACAGG 1272
Qy 733 CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGCTGCTGCTGCTGCTGCTGCTG 792
Db |
Db 1273 CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGCTGCTGCTGCTGCTGCTGCT 1332
Qy 793 TACACCGTCTTTCATGGCTTCCGCTACACCGAGTCTCAGGGAATTTGTCAGATCCAG 852
Db |
Db 1333 TACACCGTCTTTCATGGCTTCCGCTACACCGAGTCTCAGGGAATTTGTCAGATCCAG 1392
Qy 853 ATGCATTTAGATGCTCTTCACTCTCTTCCAGGATTTTGTGTCATCATATCTGT 912
Db |
Db 1393 ATGCATTTAGATGCTCTTCACTCTCTTCCAGGATTTTGTGTCATCATATCTGT 1452
Qy 913 TTCTGCAATGCTGAGGTGACGAGATTTAGGAAGTCAATGAGCGCGCTGTCAGCTGGCG 972
Db |
Db 1453 TTCTGCAATGCTGAGGTGACGAGATTTAGGAAGTCAATGAGCGCGCTGTCAGCTGGCG 1512
Qy 973 TTGACCTTCAAGCGCAAGCAAGAGTGGGAGTACAGCTACAGCTATGCGCCCAATGGTG 1032
Db |
Db 1513 TTGACCTTCAAGCGCAAGCAAGAGTGGGAGTACAGCTACAGCTATGCGCCCAATGGTG 1572
Qy 1033 TCTCACAGGTGTGACCAATTTGGGCGCGCGTGCAGACTCAGCTCCCGCTCAGCCCC 1092
Db |
Db 1573 TCTCACAGGTGTGACCAATTTGGGCGCGCGTGCAGACTCAGCTCCCGCTCAGCCCC 1632
Qy 1093 CGCTTGCCTCTGTCACATCAACATGGCCATCTCCAGCTGCTGCGCTGCGCAAGCCAGGG 1152
Db |

RESULT 2

US-08-468-249A-3
; Sequence 3, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2051 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..1846
; US-08-468-249A-3

Query Match 94.2%; Score 1243.2; DB 2; Length 2051;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 73 CTGAGGATTTTACCGCCTAGGATGATCTACACGCTGGGATATCTCAATGTCCTCGCC 132
Db |
Db 613 CGGAGGATTTTACCGCCTAGGATGATCTACACGCTGGGATATCTCAATGTCCTCGCC 672
Qy 133 TCCCTCAGGCTGGCTGCTCATCTGCGCTATTTTAGGGGCTGCACTGCACGCGCAAC 192

Db 864 GGGCTGCAGGGTGGCTGAGACCTTCTCTTCTTACTTCTTGGCCACCACTACTACTCGAT 923
Qy 429 CCTGGTGAGGGGCTGTACTTTCACAGAGCTCATCTTTCATGGCCCTTTTCTCAGAGAAGAA 488
Db 924 TCTGGTGAGGGGCTGTACTTTCACAGAGCTCATCTTTCATGGCCCTTTTCTCAGAGAAGAA 983
Qy 489 GTACTGTGGGGCTTACCACCTTCTGGTGGGGTCTACCGGCTGTCTTCTGGCTGTGTG 548
Db 984 GTACTGTGGGGCTTTCACAGCTTCTGGTGGGGTCTGCGCGCTGTCTTCTGGTGTGTG 1043
Qy 549 GGTGGGTGTACAGCAACCTTGGGCAACACATGGGTGTGGGATCTGAGCTCCGGGCAAA 608
Db 1044 GGTGAGTGTACAGCTACCTTGGGCAACACCGGGTGTGGGACTGTAGCTCCGGGAACA 1103
Qy 609 GAAGTGGATCATCAGAGTGCCCATCTGGGCACTGTGTGTCTCAACTTCATCTTTTAT 668
Db 1104 AAAGTGGATCATCAGAGTGCCCATCTGGGCTCCATTGTGTCAACTTCATCTTTTAT 1163
Qy 669 CAACATCATCCGGGTGTGTGACACTAGCTTGGGAGACCAATGGGCGCGGTGTGACAC 728
Db 1164 CAATATCTCCGGGTGTGTGACCAACAGCAGCGGGAGACCAACCGCGCGGTGTGACAC 1223
Qy 729 CAGCAGCAGTACCGGAGCTGCTCAGTCCACGTTGGTGTCTGCTGCGGCTCTTTGGTGT 788
Db 1224 ACGCAGCAGTACCGGAGCTGCTCAATCCACGCTGTGTCTCATGCCCTCTTTGGCGT 1283
Qy 789 GCACTACACCGCTTTCATGGCTTTCGCGTACACGAGGTCTCAGGGACATTTGTGGCAGAT 848
Db 1284 CCATCATATTGTCTTCATGGCCACACCATACACGAGGTCTCAGGAGCGCTTGGCAGT 1343
Qy 849 CCAGATGATATGAGATGCTTTCATCTCTCCAGGAGTATTTTGTGGCATCATATA 908
Db 1344 CCAGATGATATGAGATGCTTTCATCTCTCCAGGAGTATTTTGTGGCATCATATA 1403
Qy 909 CTGTTTCTGCAATCGTGGGTGAGGAGGATAGGAGTATAGGAGTATGAGCGGCTGGACACT 968
Db 1404 CTGTTTCTGCAATCGGAGGTGAGGAGTATAGGAGTATAGGAGTATGAGCGGCTGGACACT 1463
Qy 969 GGGCTGGAGCTTCAAGCGCAAGCAGAGTGGGAGTAGCAGCTACAGCTATGGCCCAAT 1028
Db 1464 GGCATGGACTTCAAGCGAAGGACGAGCGGAGGAGGAGCTATAGCTACGGCCCAT 1523
Qy 1029 GGTGTCTACAGAGTGTACCAATGTGGGCCCCGCTGCGAGGACTCAGCTTCCCGCTCAG 1088
Db 1524 GGTGTCTACAGAGTGTACCAATGTGGGCCCCGCTGCGAGGACTCAGCTTCCCGCTCAG 1583
Qy 1089 CCCCCGCTCTGCTGCTTACCAATGGGCACTCCAGCTGCTGGCCATGCCAA 1145
Db 1584 CCCCCGCTTACTGCTTACCAATGGGCACTCCAGCTGCTGGCCATGCCAA 1643
Qy 1146 GCCAGGGGCTCCAGCCACTGAGAC---TGAAACCTTACCAGTCACTATGGCGGTTCGCAA 1202
Db 1644 GCCAGGAGCCAGCCCTGGAGACCTTCGAGACCAACACCTGCTGCTGCTGCTCCAA 1703
Qy 1203 GGACGATGATTCCTTAAACGCTCTCTGCTCAGGCTGTGATGAGGAGGCTTCCGGGTGTC 1262
Db 1704 GGACGATGATTCCTTAAACGCTCTCTGCTCAGGCTGTGATGAGGAGGCTTCCGGGTGTC 1763
Qy 1263 GCGGCGGCTCCATTTGTGAGGAGGATGGGAAACAGTCACTGACTGGGCACTAGG 1320
Db 1764 GCGGCGGCTTCTGCTGCTACAGGAGGATGGGAGACAGTCACTGACTGGGCGCTGGG 1821

RESULT 5

US-08-468-249A-4
; Sequence 4, Application US/08468249A

; Patent No. 5886148

; GENERAL INFORMATION:

; APPLICANT: Segre et al., Gino V.

; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA

; TITLE OF INVENTION: ENCODING SAME

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2010 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..1807
; US-08-468-249A-4

Query Match 73.1%; Score 965.2; DB 2; Length 2010;

Best Local Similarity 86.6%; Pred. No. 5.9e-256;

Matches 1089; Conservative 0; Mismatches 163; Indels 6; Gaps 2;

Qy 69 TGGCTGGAGGTATTTGACCGCTTAGCATGATCTACACCGTGGGATCTCCATGTCTCT 128
Db 564 TGAACGGAGGTGTTTGACCGCTGGCATGATTTACACCGTGGGTACTCCGTGTCCCT 623
Qy 129 CGCTTCCTCAGCGTGGTGTCTCATCTGGGCTATTTTAGGGGCTGCACTGCACGG 188
Db 624 GGGTCCCTCAGCGTGGTGTCTCATCTGGGCTACTTTTAGGGGCTGCACTGCACGG 683
Qy 189 CAATCATCCACATGCACATGTTCTGTCTGTTTATGCTGCGCGCGGAGCATCTTCGT 248
Db 684 CAATCATCCACATGCACATGTTCTGTCTCTTCTGCTGCGGCGGTGAGCATCTTCGT 743
Qy 249 GAAGGAGCGTGTGCTCTTACTCTGGCTTTCAGCTGGATGAGCGCGGCTCAGAGGA 308
Db 744 CAAGGAGCGTGTGCTCTTACTCTGGCGCACGCTTGATGAGGCTGAGCGCTCAGCGGA 803
Qy 309 AGAGTTGCACATCATCGGAGGTGCCACCTCCGCGGCGGCTGCGCGCGGTAGGCTACGC 369
Db 804 GGAGTGGCGGCTATCGCCGAGCGCGGCTGCGCGCGGCTGCGCGCGCTGCGCGCTACGC 863
Qy 369 TGGCTGCGGCTGCGGCTGAGCTTCTTCTTCTTCTGCTTCTTCTGCTTCTTCTTCTGAT 428
Db 864 GGGCTGAGGGTGGCTGTGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 923
Qy 429 CTGTGTGGAGGGGCTGTACTTTGCACAGCCTCATCTTCTCATGGCCCTTTTCTCAGAGAAGAA 488
Db 924 TCTGTGTGGAGGGGCTGTACTTGCACAGCCTCATCTTCTCATGGCCCTTCTTCTCAGAGAAGAA 983
Qy 489 GTACCTGTGGGGCTTCCACCATTTTGGGTGCTACCGGCTGTCTTCTTCTTCTTCTTCTG 548

Db 1437 GCACTGCACTTCAAGCGAAGGACGACGCGGAGGAGCAGCTATAGCTAGCGCCCAT 1496
Qy 1029 GGTGTCTCACAGAGTGTGACCAATGTGGGCCCCCGTGCAGAGTCAAGCTCCCCCTCAG 1088
Db 1497 GGTGTCCACACAAAGTGTGACCAATGTGGGCCCCCGTGCAGAGTCAAGCTCCCCCTCAG 1556
Qy 1089 CCCCCG---CTGGCTCTGCGCACTACCAATGGGCACTCCAGCTGCTGGCCATGCCAA 1145
Db 1557 CCCCCGCTACTGCGCACTGCGCACTACCAAGCGCCACCTCAGCTGCTGGCCATGCCAA 1616
Qy 1146 GCCAGGGCTCCAGCACTGAGAC---TGAAACCTTACCAGTCACTATGGGGTTCCCAA 1202
Db 1617 GCCAGGACCCAGCCCTGGAGACCTCGAGACCAACACCACTGCCATGGCTGTCCCA 1676
Qy 1203 GGACGATGATTCCTTAACGGCTCTGCTCAGGCTCGATGAGGAGGCTCCGGGTCTGC 1262
Db 1677 GGACGATGGTTCCTCAACGGCTCTGCTCAGGCTCGAGGAGGAGGCTCTGGGCTGA 1736
Qy 1263 GCGGCGGCTCCATGTTGTCAGGAAGGATGGAAACAGTCACTGTA 1308
Db 1737 GCGGCCACTGCCCTGCTACAGGAAGAGTGGGAGACAGTCACTGTA 1782

RESULT 7

US-07-864-475A-2
; Sequence 2, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. (Jr.)
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; TITLE OF INVENTION: AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1863
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-864-475A-2

Query Match

52.4%; Score 691.6; DB 1; Length 1863;

Best Local Similarity 74.2%; Pred. No. 1.7e-180;
Matches 925; Conservative 0; Mismatches 294; Indels 27; Gaps 3;
Qy 73 CTGGAGGTATTGTACCGCTAGGATGATCTACACCGTGGGATACTCATCTCTCTCGCC 132
Db 629 CGGGAAGTCTTTGATCGCTCGGAATGATCTACACTGTGGGTACTCATCTCTCTCGGC 688
Qy 133 TCCCTACCGTGGGTGTGCTCATCTCGGCTATTTTATAGGCGGTGCACTGCAACGCGCAAC 192
Db 689 TCCCTACCTGTGGGTGTGCTGATTTCTGGGTACTTTTAGGAGGTATACATTTGACCGCAAC 748
Qy 193 TACATCCACATGACATGTTCCCTGTGCTTTATGTCGCGCGCGGAGCATCTTCTGTGAAG 252
Db 749 TACATTACATGACATCTCTTCTGTGCTTTATGTCGCGGCTGTAAAGCATCTTCAACAG 808
Qy 253 GACGCTGTGCTCTACTCTGCTTCAACGCTGATGAGGCGGAGCGCTCACAGAGGAAGAG 312
Db 809 GATGCTGTGCTCTACTCTGGGGTTCACAGATGAATCGAGCGCATCACCGAGGAGAG 868
Qy 313 TTGCACATCATCGCGCAGGTGCGACCTCGCGCGGCGCTGCGCGCTGAGGTACGCTGGC 372
Db 869 CTGAGGGCTTTCACAGAG-----CTTCCCTCTGTCACAGGGGGTCTTGTGGGC 919
Qy 373 TGCGCGTGGGGTGAACCTTCTTCTCTACTCTTCTGCTGCTACCACTACTACTGATCCTG 432
Db 920 TGCAGAGTGGCGGTAAACCTTCTTCTTACTTCTGACCACTACTACTGATCCTG 979
Qy 433 GTGAGGGGCTGTACTTTGACAGGCTCATCTTATGCGCTTTTCTCAGAGGAAGAATAC 492
Db 980 GTGAGGGGCTCTACTTTGACAGGCTCATCTTATGCGCTTTTCTCAGAGGAAGAATAC 1039
Qy 493 CTGTGGGGCTTTCACATCTTTGCTGGGTCTACCGGCTGTCTTCTGCTGTGTGGGTG 552
Db 1040 CTCTGGGGTTCACATTAATTTGGCTGGGGCTCTCCCTGCGGTGTTGTGCTGTGGGTG 1099
Qy 553 GGTGTGACAGCAACCTTGGCGCACTGGGTGCTGGGATCTGAGCTCGGGGCAAGAG 612
Db 1100 ACCGTGAGGGCTACACTGGCGCAACACTGAGTGTGGGACCTGAGTTCTGGGGAATAAGAAA 1159
Qy 613 TGGATCATCCAGGTGCGCCATCTTGGGCTCTGTTGTGCTCAACTTCACTCTTTTATCAAC 672
Db 1160 TGGATCATACAGGTGCGCCATCTTGGGAGCTATTTGTGGTGAATTTATCTTTTATCAAT 1219
Qy 673 ATCATCCGGTGTGCTTGCCTAAGCTTTCGGGAGACCAATCGGGCCGGTGTGACACAGG 732
Db 1220 ATAATCAGAGTCTCTGGCTACTAACTCTCGGAGACCAATGACGGGAGATGTGACACAGG 1279
Qy 733 CAGCAGTACCGGAGCTGCTCAGTCCACGTTGGTGTCTGCTGCGCTCTTTGGTGTGCAC 792
Db 1280 CAACAGTATAGAAAGCTGCTGAAGTCCACGCTAGTCTCATGCGCTATTTGGGGGTGCAC 1339
Qy 793 TACACCGTCTTTCATGGCTTTCGCTACACCGAGGTCTCAGGACATTTGTGSCAGATCCAG 852
Db 1340 TACATGCTCTTTCATGGCCACCGCTACACAGAGTATCAGGATTTCTTGGCAAGTCCAA 1399
Qy 853 ATGCATTTAGAGTGTCTTCAACTCTTCCAGGATTTTTTGTGCGCATCATATACTGT 912
Db 1400 ATGCATTTAGAAATGCTCTTCAATTTCAATTCAGGGATTTTTTGTGCGCATTTATATACTGT 1459
Qy 913 TTCTGCAATGCTGAGGTGCGGAGGAGATTTAGGAGTTCATGGAGCCGCTGAGACTGGCG 972
Db 1460 TTCTGCAATGAGAGGTGACAGCAGAGATCAAGAAGTTCATGGAGCCGATGGACCTGGCC 1519
Qy 973 TTGGACTTCAAGCGCAAGCACCAAGTGGGAGTACAGCTACAGCTATGCGCCCAATGCTG 1032
Db 1520 TTGGACTTCAAGCGCAAGCGGAGGTGGGAGGAGTACCTACAGCTATGCGCCCATGCTG 1579
Qy 1033 TCTCACACAGTGTGACCAATGTGGGCCCCCGTGCAGGAGTCTCAGCTCCCTCAGCCCC 1092
Db 1580 TCACATACAGTGTGACCAATGTGGGACCTCGAGGGGGGCTGGCGCTTGTCCCTCAGCCCT 1639
Qy 1093 CGCTGCTCTCT-----GCCACTACCAATGGCCACTCCCGAGCTGCTTGGCCATGCC 1143

Db 1640 CGACTAGCTCTGGGGCTGGAGCCAGTGCCAAATGGCCATCACCAAGTTGGCTGGCTATGTG 1699
Qy 1144 AAGCAGGGGCTCAGGCCACTGAGACTGAAACCCCTACCACTACTATGGGGTTCCTCAAG 1203
Db 1700 AAGCATGGTTCCATTTCTGAGAACTCAATGCTTTCATCTGGCCAGAGCCCTGGCACCAAA 1759
Qy 1204 GACGATGATTCCTTAAACGGCTCTGCTCAGGCCCTGAGGAGGCTCCGGGCTCTGCG 1263
Db 1760 GATCAGGGGTATCTCAATGGCTCTGG-----ACTTATGAGCCAAATGGTTGGGGAA 1810
Qy 1264 CGGCCGCTCCATTTGTCAGGAGGATGGGAAACAGTCAATGTGAC 1309
Db 1811 CAGCCCCCTCCACTCTCTGGAGGAGAGAGACAGTCAATGTGAC 1856

RESULT 8

US-08-468-249A-2
; Sequence 2, Application US/08468249A
; Patent No. 5886148

GENERAL INFORMATION:

; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992

PRIORITY INFORMATION:

; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1863 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 98...1853

US-08-468-249A-2

Query Match 52.4%; Score 691.6; DB 2; Length 1863;

Best Local Similarity 74.2%; Pred. No. 1.7e-180;

Matches 925; Conservative 0; Mismatches 294; Indels 27; Gaps 3;

Qy 73 CTGAGGATTTTACCGGCTAGGATGATCTACACCGTGGGATCTCATGTCTCTCGCC 132

Db 629 CGGGAAGTCTTTGATCGCCTCGGAATGATCTACACTGTGGGCTACTCCATCTCTCGGC 688

Qy 133 TCCCTCAGGGTGGTGTGCTCATCTCGCCTATTTTAGGCGGTGCACCTGCACCGCAAC 192

Db 689 TCCTCACTGTGGCTGTGCTGATTCTGGGTACTTTAGAGGTTACATATGCACCCGAAAC 748
Qy 193 TACATCCACATGACATGTTCTGTGTTATGCTGGCGCCGCGAGCATCTTCGTGAAG 252
Db 749 TACATTCACATGATCTCTTCTGTGCTCTTTATGCTCCGGGCTGTAAGCATCTTCATCAAG 808
Qy 253 GACGCTGTGCTCTACCTCTGCTTCAAGCTGGATGAGCGCCGAGCGCTCACAGAGGAAGAG 312
Db 809 GATGCTGTGCTCTACCTGGGGTTTCCACAGATGAAATCAGGCGCATCACCGAGGAGAG 868
Qy 313 TTGCACATCATCGCGCAGGTGCCACCTCCGCGCGGCTGCCCGCTAGGCTACGCTGGC 372
Db 869 CTGAGGGCCTTCACAGAG-----CCTCCCGCTGCTGACAAGCGGGTTTTGTGGGC 919
Qy 373 TGCCGCTGGCGGTGACCTTCTCTACTTCTGGCTACCACTACTACTGATCCTG 432
Db 920 TGCAGAGTGGCGGTAAACCGTCTTCTTACTTCTGACCAACCACTACTACTGATCCTG 979
Qy 433 GTGGAGGGGCTGTACTTGCACAGCCCTCATCTTCATGCGCTTTTCTCAGAGAAGAGTAC 492
Db 980 GTGGAAGGCTCTACCTTACAGCCTCATCTTCATGGCTTTTCTCTGAGAAAAGTAT 1039
Qy 493 CTGTGGGGCTTCAACCATCTTTTGGCTGGGTTTACCGGCTGTCTTCGTGGCTGTGTGGGTC 552
Db 1040 CTCTGGGGTTTCAATTATTTGGCTGGGCTCTCCCTGCGGTGTTGTCGTGTGGGTG 1099
Qy 553 GGTGTGAGAGCAACCTTTGGCCAACTCTGGGTGTGGGATCTGAGCTCCGGGCAACAAG 612
Db 1100 ACCGTGAGGGCTACACTGGCCAACTCTGAGTGTGGGACCTGAGTTGCGGGAAATAAGAA 1159
Qy 613 TGGATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTCACTCTTTTATCAAC 672
Db 1160 TGGATCATACAGGTGCCCATCTCTGGCAGTATTTGTGTAACCTTTATCTTTTATCAAT 1219
Qy 673 ATCATCCGGTGTCTGCCACTAAGCTTCGGGAGACCAATCGCGGCGGTGTGACACAGG 732
Db 1220 ATAATCAGAGTCTCTGGCTACTAACTCCGGGAGACCAATGACGGGAGATGTGACAGG 1279
Qy 733 CAGCAGTACCGGAAGCTGTCTCAGTCCAGTGTGGTGTCTGTGGGCTCTTTGGTGTGCAC 792
Db 1280 CAACAGTATAGAAAGCTGTCTGAAAGTCCAGCTAGTCTCATGCGGCTATTTGGGGTGCAC 1339
Qy 793 TACACGCTCTTCATGCGCTTGGCGTACACCGAGGTCTCAGGGACATTTGTGGCAGATCCAG 852
Db 1340 TACATGCTCTTCATGGCCAGCGGTACACAGAGTATCAGGGATTTCTTTGGCAAGTCCAA 1399
Qy 853 ATGCTATTAGAGATGCTCTTCAACTCTTCCAGGGATTTTGTGCCATCATATACTGT 912
Db 1400 ATGCACTATGAAATGCTCTTCAATTCATTCAGGGATTTTTCGTGGCATTATATACTGT 1459
Qy 913 TTCTGCAATGGTGAAGTGCAGGAGATAGGAAGTATAGGAAGTATGAGACCGCTGGACACTGGCG 972
Db 1460 TTCTGCAATGGAGAGTACAAAGAGATCAAGAAGTCAAGAGCCGATGGAGCCCTGGCC 1519
Qy 973 TTGAGCTTCAAGCGCAAGCAACGAAGTGGGAGTAGCAGCTACAGCTATATGGCCCAATGGTG 1032
Db 1520 TTGAGCTTCAAGCGGAAGGCCCGGAGTGGCAGCAGTACCTACAGCTATATGGCCCATGGTG 1579
Qy 1033 TCTCACAAGAGTGTGACCAATGTGGGCCCCCGGTGACGAGTCAAGCTCTCCCTTCAGCCCC 1092
Db 1580 TCACATACAAAGTGTCAACCAATGTGGGACCTCGAGGGGGGCTGGCTTGTCCCTCAGGCCCT 1639
Qy 1093 CGCTGCTCTCT-----GCCATCAAGTGGCCATCCAGCTGCTGGCCATGCC 1143
Db 1640 CGACTAGTCTCTGGGCTGGAGCCAGTGCCCAATGGCCATCCAGTTGCTGGCTATGTG 1699
Qy 1144 AAGCAGGGGCTCCAGCACTGAGAGCTGAAACCTTACCACTACTATGGCGGTTTCCCAAG 1203
Db 1700 AAGCATGGTTCCATTTCTGAGAACTCATTTGCCCTTCATCTGGCCAGAGCCCTGGCACCAAA 1759
Qy 1204 GACATGATGATTCCTTAAACGGCTCTCTGCTCAGGCTGGATGAGAGGCTCTCGGGTCTGCG 1263

Db 1760 GATGACGGGTATCTCAATGGCTCTGG-----ACTTATGAGCCAAATGGTTGGGGAA 1810
Qy 1264 CGCGCGCTCCATTTGTTGAGGAAGATGGGAAACAGTCAATGTGAC 1309
Db 1811 CAGCCCCCTCCACTCTCTGGAGGAGAGAGACAGTCAATGTGAC 1856

RESULT 9

US-07-864-475A-1
; Sequence 1, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. (Jr.)
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; TITLE OF INVENTION: AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1862
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-07-864-475A-1
Query Match 51.6%; Score 681.2; DB 1; Length 1862;
Best Local Similarity 74.2%; Pred. No. 1.3e-177;
Matches 925; Conservative 0; Mismatches 293; Indels 28; Gaps 4;
Qy 73 CTGAGGATATTTGACCGCCCTAGGCATGATCTACACCGTGGGATCTCCATGTCTCTCGCC 132
Db 629 CGGGAAGTCTTTGATCGCCTCGGAATGATCTACACTGTGGGTACTCCATCTCTCTGGC 688
Qy 133 TCCCTACCGTGGTGTGCTCATCTCGCCCTATTTAGGCGGTGCTGACCTGACCGCAAC 192
Db 689 TCCCTCACTGTGGTGTGCTGATCTCGGGTACTTTAGGAGTTTACATTGACCCGAAAC 748
Qy 193 TACATCACATGACATGTTCTCTGTCTTTATGCTGCGCGCGGAGCATCTTCTGTGAAG 252
Db 749 TACATTACATGACATCTCTCTGTGTCCTTTATGCTCCGGGTGTAAAGCATCTTCATCAAG 808
Qy 253 GAGCGTGTGCTCTACTCTGGCTTCACTGAGTGGAGCGCGCTTACAGAGGAAGAG 312

Db 809 GATGCTGTGCTCTACTCGGGGTTTCCACAGATGAAATCGAGCGCATCACCGAGGAGAG 868
Qy 313 TTGCACATCATCGCGAGGTGCGACCTCGCGCGCGCTCGCGCGGTAGCTAGCTGCTGGC 372
Db 869 CTGAGGGCCTTACAGAG-----CCTCCCTGCTGACGAAGCGGGTTTGTGGGC 919
Qy 373 TGCGCGTGGCGGTGACCTTCTCTCTACTTCTGCTACTTCTGCTACCAACTACTACTGATCCTG 432
Db 920 TGACAGAGTGGCGGTAAACCGTCTTCTTACTTCTGACCAACCACTACTACTGATCCTG 979
Qy 433 GTGAGGGGCTGTACTTGCACAGCCTCATCTTCAATGGCCTTTTCTCAGAGAGAGACTAC 492
Db 980 GTGGAAGGCTCTACCTTTCACAGCCTCATCTTATGGCTTTTCTCTGAGAAAAAGTAT 1039
Qy 493 CTGTGGGGCTTACCACTTCTTGGCTGGGGTCTACCGGCTGCTTCTGTGGGCTGTGTGGGTC 552
Db 1040 CTCTGGGGTTTCACTATTTTGGCTGGGGCTCTCCCTGCGGTGTTGTGCTGTGTGGGTG 1099
Qy 553 GGTGTGAGAGCAACCTTGGCCAACTGCGGTGCTGGGATCTGAGCTCGGGGCAAGAAG 612
Db 1100 ACGTGGGGCTACACTGGCCAACTGAGTGTGGGACCTGAGTTCGGGGAATAAGAAA 1159
Qy 613 TGGATCATCCAGGTGGCCATCTCTGGCATCTGTTGTGCTCACTTCTCTTATCAAC 672
Db 1160 TGGATCATACAGGTGGCCATCTCTGGCAGCTATTGTGTGTAACCTTATCTTTTATCAAT 1219
Qy 673 ATCATCGGGTGTCTGCCACTAAGCTTTCGGGAGACCAATCGCGGCGGTGTGACACAGG 732
Db 1220 ATATCAGAGTCTCTGGTACTTAACTCCGGGAGACCAATGACGGAGATGTGACACAGG 1279
Qy 733 CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTCTCGTCCGCTCTTTTGGTGTGAC 792
Db 1280 CAACAGTATAGAAAGCTGCTGAAAGTCCACGCTAGTCTCTCATGCGCTATTTTGGGTGCAC 1339
Qy 793 TACACGCTCTTATGGCTTGCCTGACACCGAGGTCTCAGGAGCATTTGCGGAGATCCAG 852
Db 1340 TACATGCTCTTATGGCCACCGCTGACACAGAAAGTATCAGGGGATTTCTTTGGCAAGTCCAA 1399
Qy 853 ATGCTATTATGAGATGCTCTTCAACTCTTCCAGGGATTTTGTGTCATCATATCTGT 912
Db 1400 ATGCTATTATGAGATGCTCTTCAATTTCAATCCAGGGATTTTGTGTCATATATATCTGT 1459
Qy 913 TTCTGCAATGGTGGGTGAGGTGAGGAGATTTAGGAAGTCAATGAGCGCTGAGACATCTGGCG 972
Db 1460 TTCTGCAATGGAGAGGTACAAAGCAGAGATCAAGAAGTCAATGAGCGGATGACCCCTGGCC 1519
Qy 973 TTGGACTTCAAGCGGAAAGCAAGAGTGGAGTAGCAGCTACAGCTATGCCCCCAATGGTG 1032
Db 1520 TTGGACTTCAAGCGGAAAGCCCGAGTGGCAGCAGTACCTACAGCTATGCCCCCATGGTG 1579
Qy 1033 TCTTCACAGAGTGTGACCAATGTTGGGCCCGCGTGCAGGACTCAGCCTCCCCCTCAGCCCC 1092
Db 1580 TCACATACAGTGTCCCAATGTTGGGACCTCGAG-GGGGCTGGCTTGTCTCTCAGCCCT 1638
Qy 1093 CGCTGCTCTCT-----GCCACTACCAATGGCCACTTCCAGAGTCTCTCCCTGCGCATGCC 1143
Db 1639 CGACTAGCTCTGGGGCTGGAGCCAGTGCAATGGCCATCACCAGTTGCTGTGCTATGTG 1698
Qy 1144 AAGCCAGGGGCTCCAGCCACTGAGACTGAAACCCCTACAGTCACTATGCGGGTTCCTCAAG 1203
Db 1699 AAGCATGGTTCCATTTCTGAGAACTCATTTGCCCTTCTATCTGGCCAGAGCCTGGCACCAA 1758
Qy 1204 GAGATGAGTCTCTTAACGGCTCTCTCAGGCGCTGGATGAGGAGGCTCCCGGCTCTGCG 1263
Db 1759 GATGAGGGGTATCTCAATGGCTCTGG-----ACTTATGAGCAATGGTTGGGAA 1809
Qy 1264 CGCGCGCTCTCATTTGTTGAGGAAGGATGGGAAACAGTCAATGTGAC 1309
Db 1810 CAGCCCCCTCCACTCTCTGGAGGAGAGAGACAGTCAATGTGAC 1855


```
Db 560 TTCTTGGCTGTGGCTATTCTCATCATTTGGTTACTTCAGACGATTGCACTAGGAA 619
Qy 192 CTACATCCACATGACATGTTCTGTGTTATGCTGCGCGCGCGAGCATCTTCTGGAA 251
Db 620 CTATATCCACATGACATTAATTTGTGTTCTTCATGCTGAGAGCTACAAAGCATCTTTGTCAA 679
Qy 252 GGAGCGTGTGCTTACTCTGGCTTTCAGCTGGATGAGCGCGAGCGCTTCACAGAGGAGA 311
Db 680 AGACAGAGTAGTCATGCTCACATAGGAGTAAGAGAGCTGGAGTCCCTAATAATGACGGA 739
Qy 312 GTTCCACATCATCCGCGAGGTGCCACCTCGCGCGCGCGCTGCCCGCTAGGCTACGCTGG 371
Db 740 TGACCCCAAAATTCATAGGCAACTTCTGTGGCAAAATC-----ACAAATATATCGG 793
Qy 372 CTGCGCGGTGGCGTGACCTTCTTCTCTACTCTTCTGGCTACCAACTACTACTGGAATCCT 431
Db 794 GTGCAAGATTGCTGTTGTGATGTTTAACTTCTGGCTACAAATTAATTTGGATCCT 853
Qy 432 GGTGGAGGGCTGTACTTGTGACAGCTCATCTTCATGCGCTTTTCTCAGAGAGAGTA 491
Db 854 GGTGGAAGGCTCTACCTGCGAATACTCATCTTGTGGCTTTCTTTTGGACACCAATA 913
Qy 492 CCTGTGGGGCTTACCACTCTTTGGCTGGGGTCTACCGGCTGTCTTCTGGCTGTGGGT 551
Db 914 CCTGTGGGGCTTCACTTGTAGAGCTGGGGTTTCCAGCAGCAATTTGTTGCAGCATGGC 973
Qy 552 CGGTGTGAGAACACCTTGGCAACACATGGGTGCTGGGATCTGAGCTCGCGGCAAGAA 611
Db 974 TGTGGCACGAGCAACTGTGGCTGATGCGAGGTCTGGGAACCTAGTCTGGAGACATCAA 1033
Qy 612 GTGATCATCCAGGTGCCATCTGCGATCTGTGTGCTCAACTTCATCTCTTTTATCAA 671
Db 1034 GTGGAATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAAATTTTATCTGTCTGAA 1093
Qy 672 CATCATCCGGGTCTTGGCAACTAAGCTTGGGAGACCAATGCGGGCGGTGTGACACCAG 731
Db 1094 TACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAATGAGTGGGATGACAA 1153
Qy 732 GCAGCAGTACCGAAGCTGTCTAGGTCCAGCTTGGTGTGCTGTCGCGCTCTTTGTGTGCA 791
Db 1154 GAAGCAATACAGGAAACTGGCAAAATCGACACTGGTCTGCTCTAGTCTTTGGAGTGCA 1213
Qy 792 CTACACGCTTTCATGCGCTTGGCTACCGAGTCTCAGGAGACATTTGGGACAGATCCA 851
Db 1214 TTACATCGTGTGTGCTGCGCTCCTCACTCC---TTCACTGGGCTCGGGTGGGAGATCCG 1270
Qy 852 GATGCATTATGAGATGCTCTTCAACTCTTCCAGGGAATTTTTTGTGCCATCATATACTG 911
Db 1271 CATGCACTGTGAGCTCTTCTTCACTCTTTCAGGGTTTCTTTGTGTCTATCATCTACTG 1330
Qy 912 TTTCTGCAATGGTGTGAGGTGAGGAGAGATTAGGAAGTCAATGGAGCGCTGGACATGGC 971
Db 1331 CTACTGCAATGGAGAGTTTCAAGCAGAGGTGAAGAGATGTGAGTGGGTGGAATCTCTC 1390
Qy 972 GTTGGACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCT 1018
Db 1391 CGTGGACTGGAAGGACACCGCCATGTGGAGCGCGCAGATGCGGCT 1437
```

RESULT 13

US-09-236-468A-1

; Sequence 1, Application US/09236468A

; Patent No. 6338951

; GENERAL INFORMATION:

; APPLICANT: Soppet et al.

; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTGD74

; FILE REFERENCE: P201D1

; CURRENT APPLICATION NUMBER: US/09/236,468A

; CURRENT FILING DATE: 1999-01-25

; PRIOR APPLICATION NUMBER: 08/468,011

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2003

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (90) ..(1715)

US-09-236-468A-1

Query Match

Best Local Similarity 29.3%; Score 387.4; DB 3; Length 2003;

Matches 612; Conservative 0; Mismatches 326; Indels 9; Gaps 2;

```
Qy 72 GCTGGAGGTATTGACGGCTTAGGCATGATCTACACGGTGGGATACCTCATGCTCTCTCGC 131
Db 500 GCAAGAATTTCTGTGAACGGCTCTATGTAATGTATACCGTTGGCTACTCCATCTCTTTGG 559
Qy 132 CTCCTTCACGGTGGCTGTGCTCATCTCTGGCTATTTTAGCGGCTGCACCTGCACGGGCAA 191
Db 560 TTCTTGGCTGTGGCTATTCTCATCATTTGGTTACTTCAGACGATTGCACTAGGAA 619
Qy 192 CTATATCCACATGACATGTTCTGTGTTTATGCTGCGCGCGAGCATCTTCTGGAA 251
Db 620 CTATATCCACATGACATTAATTTGTGTTCTTCATGCTGAGAGCTTACAAGCATCTTTGTCAA 679
Qy 252 GGAGCGTGTGCTTACTCTGGCTTTCAGCTGGATGAGCGCGAGCGCTTCACAGAGGAGA 311
Db 680 AGACAGAGTAGTCCATGCTCACATAGGAGTAAGAGAGCTGGAGTCCCTAATAATGACGGA 739
Qy 312 GTTGCACATCATCGCGAGGTGCCACTCGCGCGCGCTGCCCGCTAGGCTACGCTGG 371
Db 740 TGACCCCAAAATTCATAGGCAACTTCTGTGGCAAAATC-----ACAAATATATCGG 793
Qy 372 CTGCGCGGTGGCGTGACCTTCTTCTCTACTCTTCTGGCTTACCAACTACTACTGGAATCCT 431
Db 794 GTGCAAGATTGCTGTTGTGATGTTTAACTTCTGGCTACAAATTAATTTGGATCCT 853
Qy 432 GGTGGAGGGCTGTACTTGTGACAGCTCATCTTCATGCGCTTTTCTCAGAGAGAGTA 491
Db 854 GGTGGAAGGCTCTACTCTGCAATCTCATCTTGTGTGGCTTTCTTTTGGACACCAATA 913
Qy 492 CCTGTGGGGCTTCAACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCTGGCTGTGGGT 551
Db 914 CCTGTGGGGCTTCACTTGTAGAGCTGGGGTTTCCAGCAGCAATTTGTTGCAGCATGGC 973
Qy 552 CGGTGTGAGAACACCTTGGCAACACATGGGTGCTGGGATCTGAGCTCGCGGCAAGAA 611
Db 974 TGTGGCACGAGCAACTGTGGCTGATGCGAGGTCTGGGAACCTAGTCTGGAGACATCAA 1033
Qy 612 GTGATCATCCAGGTGCCATCTGCGATCTGTGTGCTCAACTTCATCTCTTTTATCAA 671
Db 1034 GTGGAATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAAATTTTATCTGTCTGAA 1093
Qy 672 CATCATCCGGGTCTTGGCAACTAAGCTTGGGAGACCAATGCGGGCGGTGTGACACCAG 731
Db 1094 TACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAATGAGTGGGATGACAA 1153
Qy 732 GCAGCAGTACCGAAGCTGTCTAGGTCCAGCTTGGTGTGCTGTCGCGCTCTTTGTGTGCA 791
Db 1154 GAAGCAATACAGGAAACTGGCAAAATCGACACTGGTCTGCTCTAGTCTTTGGAGTGCA 1213
Qy 792 CTACACGCTTTCATGCGCTTGGCTACCGAGTCTCAGGAGACATTTGGGACAGATCCA 851
Db 1214 TTACATCGTGTGTGCTGCGCTCCTCACTCC---TTCACTGGGCTCGGGTGGGAGATCCG 1270
Qy 852 GATGCATTATGAGATGCTCTTCAACTCTTCCAGGGAATTTTTTGTGCCATCATATACTG 911
Db 1271 CATGCACTGTGAGCTCTTCTTCACTCTTTCAGGGTTTCTTTGTGTCTATCATCTACTG 1330
Qy 912 TTTCTGCAATGGTGTGAGGTGAGGAGAGATTAGGAAGTCAATGGAGCGCTGGACATGGC 971
Db 1331 CTACTGCAATGGAGAGTTTCAAGCAGAGGTGAAGAGATGTGAGTGGGTGGAATCTCTC 1390
Qy 972 GTTGGACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCT 1018
Db 1391 CGTGGACTGGAAGGACACCGCCATGTGGAGCGCGCAGATGCGGCT 1437
```


Qy 972 GTTGACATTCAGCGCAAGCAACGAGTGGAGTAGCAGCTACAGCT 1018
|||||
Db 1391 CGTGGAGTAAAGGACACCGCCATGTGGCGCGCAGATGCGCT 1437

RESULT 14

PCT-US95-07085-1

; Sequence 1, Application PC/TUS9507085

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R

; APPLICANT: Yi, Li

; APPLICANT: Rosen, Craig A

; APPLICANT: Ruben, Steven

; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor

; TITLE OF INVENTION: HLTG74

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,

; ADDRESSEE: Stewart & Olstein

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: NJ

; COUNTRY: USA

; ZIP: 07068-1739

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/07085

; FILING DATE: 05-JUN-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: MULLINS, J.G.

; REGISTRATION NUMBER: 33,073

; REFERENCE/DOCKET NUMBER: 325800-393

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2003 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 90..1712

PCT-US95-07085-1

Query Match 29.3%; Score 387.4; DB 5; Length 2003;
Best Local Similarity 64.6%; Pred. No. 1.5e-96;
Matches 612; Conservative 0; Mismatches 326; Indels 9; Gaps 2;

Qy 72 GCTGGAGTATTGACCGCTAGGACATCTACACGCTGGGATCTCCATGCTCTCGC 131
|||
Db 500 GCAAGATCTGTGAACGCTCTATGTAAATGATATACCGTTGGCTACTCCATCTCTTTGG 559
|||
Qy 132 CTCCTCCACGCTGGCTGTGCTCATCTGGCCCTATTTTAGGGGCTGCACTGCACGCGCAA 191
|||
Db 560 TTCCTGGCTGGCTATCTCATCATCTGGTTACTTCAGACGATTCGATTCAGTACAGGAA 619
|||
Qy 192 CTACATCCACATGACATGTTCTGTTGTTATGCTGGCGCGCGGAGCATCTTCGTGAA 251
|||
Db 620 CTATATCCACATGACATCTATTTGTTGTTCTTCATGCTGAGAGCTACAAGCATCTTTGTCAA 679
|||
Qy 252 GGACGCTGTGCTTACTCTGCTTTCACGCTGATGAGCGCGGAGCTCAGAGGAGA 311
|||
Db 680 AGACAGAGTAGTCCATGCTCACAAGGAGTAAAGGAGCTGGAGTCCCTTAATAATGACGGA 739
|||

Qy 312 GTTGACATCATCGCGCAGGTGCCACTCGCGCGCGCTGCGCGCTAGGCTAGCTGG 371
|||
Db 740 TGACCCCAAAATTCATTGAGGCAACTTCGTGGACAAATC-----ACAAATATATCGG 793
|||
Qy 372 CTGCGCGTGGCGGTGACCTTCTCTCTACTTCTCTGGCTACCAACTACTACTGGATCCT 431
|||
Db 794 GTGCAAGATTGCTGTTGTGATGTTTATTACTTCTCTGGCTACAAATATTATTGGATCCT 853
|||
Qy 432 GGTGGAGGGCTGTACTTTGCACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGAATA 491
|||
Db 854 GGTGGAAGGTCTCTACCTGCATAATCTCATCTTTGTGGCTTTCTTTTCGGACACCAATA 913
|||
Qy 492 CCTGTGGGCTTCAACCATCTTTGGCTGGGCTCTACCGGCTGTCTCTGGTGGCTGTGGT 551
|||
Db 914 CCTGTGGGCTTTCATCTTGATGGCTGGGGGTTTCCAGCAGCATTTGTTTCAGCATGGC 973
|||
Qy 552 CGGTGTGAGCAACCTTTGGCCAACTGCGGTGCTGGGATCTCAGAGCTCGGGGCAACAAGAA 611
|||
Db 974 TGTGGCAGAGCACTCTGCTGATGGAGTGTCTGGAACTTAGTCTGGAGACATCAA 1033
|||
Qy 612 GTGGATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTCATCTTTTATCAA 671
|||
Db 1034 GTGGATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAAATTTTATTCTGTTCTGAA 1093
|||
Qy 672 CATCATCCGGTGTGCTGCCACTAAGCTTCGGGAGACCAATCGCGGCGGTGTGACACAG 731
|||
Db 1094 TACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAATTTGGGCAATGACACAAG 1153
|||
Qy 732 GCAGCAGTACCGAAGCTGCTCAGGTCCACGTTGGTGTCTCGTGGCTCTTTGGTGTGCA 791
|||
Db 1154 GAAGCAATACAGAACTGGCCAAATGACACTGGTCTCTGCTCTAGTCTTTGGAGTGA 1213
|||
Qy 792 CTACACCGTCTTCATGGCTTGGCGTACACCGAGGTCTCAGGGACATTTGGCAGATCCA 851
|||
Db 1214 TTACATCGTGTGCTGCTGCTCCTCCTCC---TTCACCTGGGCTCGGGTGGGAGATCCG 1270
|||
Qy 852 GATGCATTATGAGATGCTCTTCAACTCTTCAGGGGATTTTGTGTCGCAATATATCTG 911
|||
Db 1271 CATGCACTGTGAGCTCTTCTTCAACTCTTTCAGGGTTCCTTTGTGCTATCATCTACTG 1330
|||
Qy 912 TTTCTGCAATGTGAGTGCAGGACAGATTTAGGAATCATGAGCGGCTGGACACATGGC 971
|||
Db 1331 CTACTGCAATGGAGAGTTTCAGGACAGGTGAAGAGATGTGAGTGGTGGATCTCTC 1390
|||
Qy 972 GTTGGACTTCAAGCGCAAGACAGAAAGTGGGAGTAGCAGCTACAGCT 1018
|||
Db 1391 CGTGGACTGGAAGGACACCGCATGTGCGAGCCGACAGATGCGGCT 1437
|||

RESULT 15

US-09-449-632-3

; Sequence 3, Application US/09449632

; Patent No. 6541220

; GENERAL INFORMATION:

; APPLICANT: Jppner, Harald

; APPLICANT: Rubin, David A.

; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof

; FILE REFERENCE: 0609 4740001/SRL/W-G

; CURRENT APPLICATION NUMBER: US/09/449,632

; CURRENT FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: US 60/110,467

; PRIOR FILING DATE: 1998-11-30

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 2152

; TYPE: DNA

; ORGANISM: zebrafish

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (394)..(2019)

; NAME/KEY: misc feature

; LOCATION: (2125)..(2125)

OTHER INFORMATION: n is any nucleotide of a,t,g or c
US-09-449-632-3

Query Match 29.3%; Score 387.4; DB 4; Length 2152;
Best Local Similarity 65.4%; Pred. No. 1.5e-96;
Matches 608; Conservative 0; Mismatches 276; Indels 45; Gaps 1;

Qy	68	ATGCGCTGGAGGATTTGACCGCTAGGCATGATCTACACGGTGGGATCTCCATGTCTC	127
Db	791	ATCAGGAGGAAGTGTGAGCGCTTTACCTCATGTACACTATTGGATCTCCATATCAC	850
Qy	128	TGCGCTCCCTCACGGTGGTGTCTCATCTGGGCTATTTTAGCGGCTGCACCTGCACGC	187
Db	851	TGGCAGGTTACTGGTGGGCTCTATCTCTTTGCTATTTCAACGCTCCACTGCACCTC	910
Qy	188	GCAACTACATCCACATGACATGTTCTCTGCTGTTTATGCTGCGCGCCGAGCATCTTCG	247
Db	911	GTAATAATCCACATCCACCTCTTACCTCGTTTATATGTCGAGCAATCAGTATTTTG	970
Qy	248	TGAAGGAGGCTGCTCTACTCTGCTTACCGCTGATGAGCGGAGCGCTCACAGAGG	307
Db	971	TGAAAGACGCGGTTCTTTACGCGCTCAGAAATGATGGAGAACTAGAAAGATGGGCGAGTGG	1030
Qy	308	AAGAGTTGCACATCATCGCGAGGTGCCACCTCGCGCGCGCTGCGCGTAGGCTACG	367
Db	1031	AACAAAGACCAT-----GG 1045	
Qy	368	CTGGCTCGCGGTGGCGGTGACCTTCTTCCTCTACTTCTGGGTACCAACTACTACTGA	427
Db	1046	TGGGCTGCAAGGCTGCTGTGACCCCTTCTCTGTATCTGTGGGACCAATCATTTATTGA	1105
Qy	428	TCCGTGGTGGAGGCTGTACTTGCACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGA	487
Db	1106	TCCTGGTGGAGGTTGTACTTGCATAGTCTGATCTTTCATGGCCCTCTCTGCTGTGATAAGA	1165
Qy	488	AGTACCTGTGGGCTTCCACATCTTGGCTGGGCTCTACCGGCTGTCTTGGTGGCTGTGT	547
Db	1166	ACTGCTGTGGGCTTTGACAAATCATAGCTGGGGATCCACAGCAGTGTGTTGTGTCTATAT	1225
Qy	548	GGGTGGTGTGAGAGCAACCTTGGCCAACTGGGTGCTGGGATCTGAGCTCCGGGCACA	607
Db	1226	GGGTGAGTGGAGTCCAGGTGCCATCTCTGGCAGACACAGTGTCTGGGATATCAGTGCAGGCAATT	1285
Qy	608	AGAAGTGGATCATCCAGGTGCCATCTCTGGCAGTCTGTGCTCAACTTCATCTCTTTTA	667
Db	1286	TGAAATGGATTTATCAAGTACCAATCTCGGAGCCATTTGTTAAACTTCTCTCTCTCC	1345
Qy	668	TCAACATCATCGGGTGTCTGCCACTAAGCTTCGGGAGACCAATCGCGGCGGTGTGACA	727
Db	1346	TCAATATCATCAGGGTTTGGCCCTTAAGTTGTGGGAAACAAACACGGGAAACTGGACC	1405
Qy	728	CCAGGACGAGTACCGGAAGCTGTCTCAGGTCCACGTTGGTGTCTCGTCCGCTCTTTGGTG	787
Db	1406	CTAGACAGCAGTACAGGAAGCTGTGAAGTCAACAATGGTGTCTGATGCCACTGTTGGAG	1465
Qy	788	TGCATACACCGTCTTTCATGSCCTTGGCTGACCGAGGCTCAGGACATTGTGGCAGA	847
Db	1466	TTCAATACATCTGTCTCATGGCTCTTCGGTACACTGATGTGACTGGTTGCTGAGGCAGA	1525
Qy	848	TCCAGATGCATTTATGAGATGCTTTCAACTCTTCCAGGGATTTTGTGTCATCATAT	907
Db	1526	TTCTGATGATACAGATGCTCTTCAATCTTTCACAGGGTTCTTTGTGGGCTTTATTT	1585
Qy	908	ACTGTTTCTGCAATGGTGGTGGAGTGCAGGAGAGATTTAGGAAGTCAATGAGCGCGCTGGACAC	967
Db	1586	ACTGCTTCTGCAATGGGAGGTGCAGGAGAGGTGAAGAAGGCTGTGTTGCGACGAGTC	1645
Qy	968	TGGCGTTGGACTTCAAGCGCAAGCAGA 996	
Db	1646	TTGCGTTAGACCTGAAGCAGAAGGCTCGA 1674	

Job time : 260 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 4, 2005, 01:28:13 ; Search time 2710 Seconds
(without alignments)
3055.086 Million cell updates/sec

Title: US-09-869-565-1,
Perfect score: 1320
Sequence: 1 atgggggcccgcggatgcg.....tcattgtactgggcaactagg 1320

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10J_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243.2	94.2	2051	16	US-10-267-730-3 Sequence 3, Appli
2	1241.6	94.1	2065	18	US-10-152-319A-1741 Sequence 1741, Ap
3	1229.6	93.2	1776	9	US-09-943-446-3 Sequence 3, Appli
4	1146.4	86.8	1776	9	US-09-943-446-4 Sequence 4, Appli
5	1146.4	86.8	1776	9	US-09-943-446-5 Sequence 5, Appli
6	966.8	73.2	1948	15	US-10-225-567A-228 Sequence 228, App
7	966.8	73.2	1948	17	US-10-305-720-1253 Sequence 1253, Ap

8	966.8	73.2	1948	21	US-10-956-157-395 Sequence 395, App
9	966.8	73.2	2282	20	US-10-723-860-5567 Sequence 5567, Ap
10	965.2	73.1	2010	16	US-10-267-730-4 Sequence 4, Appli
11	965.2	73.1	2171	20	US-10-723-860-1005 Sequence 1005, Ap
12	959.6	72.7	1782	10	US-09-826-509-562 Sequence 562, App
13	959.6	72.7	1782	21	US-10-925-095-562 Sequence 562, App
14	958.2	72.6	1779	21	US-10-505-486-14 Sequence 14, Appli
15	902.2	68.3	2177	9	US-09-943-446-1 Sequence 2, Appli
16	899	68.1	1788	9	US-09-943-446-2 Sequence 1564, Ap
17	758.4	57.5	2192	17	US-10-062-674-1564 Sequence 2, Appli
18	691.6	52.4	1863	16	US-10-267-730-2 Sequence 1, Appli
19	681.2	51.6	1862	16	US-10-267-730-1 Sequence 229, App
20	610.8	46.3	1609	16	US-10-332-859-229 Sequence 1, Appli
21	554.6	42.0	1609	18	US-10-372-095-1 Sequence 9, Appli
22	462.4	35.0	637	18	US-10-332-859-9 Sequence 523, App
23	387.4	29.3	1896	17	US-10-295-027-523 Sequence 1, Appli
24	387.4	29.3	2003	9	US-09-996-569-1 Sequence 1, Appli
25	387.4	29.3	2003	21	US-10-921-218-1 Sequence 3, Appli
26	387.4	29.3	2152	16	US-10-372-095-3 Sequence 226, App
27	387.4	29.3	2641	15	US-10-225-567A-226 Sequence 525, App
28	387.4	29.3	2641	17	US-10-295-027-525 Sequence 850, App
29	387.4	29.3	2641	17	US-10-295-027-850 Sequence 1463, Ap
30	387.4	29.3	2641	17	US-10-305-720-1463 Sequence 70, Appli
31	387.4	29.3	2641	19	US-10-283-975A-70 Sequence 2138, Ap
32	387.4	29.3	2641	20	US-10-723-860-2138 Sequence 6394, Ap
33	387.4	29.3	3071	20	US-10-723-860-6394 Sequence 564, App
34	385.8	29.2	1653	10	US-09-826-509-564 Sequence 564, App
35	385.8	29.2	1653	21	US-10-925-095-564 Sequence 5630, App
36	331.6	25.1	600	21	US-10-956-157-5630 Sequence 392, App
37	328.6	24.9	343	17	US-10-062-674-392 Sequence 709, App
38	265	20.1	21704	15	US-10-017-161-709 Sequence 621, App
39	265	20.1	21704	17	US-10-292-798-621 Sequence 104, App
C 40	241.8	18.3	509	11	US-09-968-007A-104 Sequence 336, App
C 41	241.8	18.3	509	11	US-09-968-007A-336 Sequence 724, App
C 42	241.8	18.3	509	11	US-09-968-007A-724 Sequence 6574, Ap
C 43	241.8	18.3	509	21	US-10-843-641A-5574 Sequence 6806, Ap
C 44	241.8	18.3	509	21	US-10-843-641A-6806 Sequence 7194, Ap
C 45	241.8	18.3	509	21	US-10-843-641A-7194

ALIGNMENTS

RESULT 1

- US-10-267-730-3
- Sequence 3, Application US/10267730
- Publication No. US20030153041A1
- GENERAL INFORMATION:
- APPLICANT: Segre, Gino V.
- APPLICANT: Kronenberg, Henry M.
- APPLICANT: Abou-Samra, Abdul-Badi
- APPLICANT: Juppner, Harald
- APPLICANT: Potts, Jr., John T.
- APPLICANT: Schipani, Ernestina
- TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
- FILE REFERENCE: 00786/071005
- CURRENT APPLICATION NUMBER: US/10/267,730
- CURRENT FILING DATE: 2003-01-27
- PRIOR APPLICATION NUMBER: US 08/471,494
- PRIOR FILING DATE: 1995-06-06
- NUMBER OF SEQ ID NOS: 28
- SOFTWARE: FastSeq for Windows Version 4.0
- SEQ ID NO 3
- LENGTH: 2051
- TYPE: DNA
- ORGANISM: Rattus rattus
- FEATURE:
- NAME/KEY: CDS
- LOCATION: (73)...(1845)
- US-10-267-730-3

Query Match 94.2%; Score 1243.2; DB 16; Length 2051;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Qy	73	CTGAGAGTATTGACCGCCTAGGCAATGATACACCGTGGGATCTCATGTCTCTCGCC	132						
Db	613	CGGAGGATATTGACCGCCTAGGCAATGATACACCGTGGGATCTCATGTCTCTCGCC	672						
Qy	133	TCCCTCAGCGTGGCTGTGCTCATCTGCGCTATTATTTAGGCGGCTGCACTGCACGCGCAAC	192						
Db	673	TCCCTCAGCGTGGCTGTGCTCATCTGCGCTATTATTTAGGCGGCTGCACTGCACGCGCAAC	732						
Qy	193	TACATCCACATGCAATGTTCTCTGCTTTATGCTGCGCGCGGAGCATCTTCTGTGAAG	252						
Db	733	TACATCCACATGCAATGTTCTCTGCTTTATGCTGCGCGCGGAGCATCTTCTGTGAAG	792						
Qy	253	GACGCTGCTCTACTCTGGCTTACGCTGATGAGCGCGGCTTACAGAGGAAGAG	312						
Db	793	GACGCTGCTCTACTCTGGCTTACGCTGATGAGCGCGGCTTACAGAGGAAGAG	852						
Qy	313	TTGCACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCGCGGTAGGCTACGCTGGC	372						
Db	853	TTGCACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCGCGGTAGGCTACGCTGGC	912						
Qy	373	TGCGCGGTGGCGGTGACCTTCTCTCTACTTCTGCTACCACTACTACTACTGATCCTG	432						
Db	913	TGCGCGGTGGCGGTGACCTTCTCTCTACTTCTGCTACCACTACTACTACTGATCTG	972						
Qy	433	GTGAGGGGTGTACTTGCACAGGCTCATCTTATGCGCTTTTCTCAGAGAAGATAC	492						
Db	973	GTGAGGGGTGTACTTGCACAGGCTCATCTTCTATGCGCTTTTCTCAGAGAAGATAC	1032						
Qy	493	CTGTGGGCTTCAACATCTTTGGCTGGGCTCTACCGCTGTCTTCTGTGGCTGTGGTC	552						
Db	1033	CTGTGGGCTTCAACATCTTTGGCTGGGCTCTACCGCTGTCTTCTGTGGCTGTGGTC	1092						
Qy	553	GGTGTGAGAGCAACCTTTGGCCAAACACTGGGTCTGGGATCTGAGCTCCGGGCAAGAAG	612						
Db	1093	GGTGTGAGAGCAACCTTTGGCCAAACACTGGGTCTGGGATCTGAGCTCCGGGCAAGAAG	1152						
Qy	613	TGGATCATCAGGTGCCATCTGGGATCTGTGTGCTCAACTTCATCTTTTATCAAC	672						
Db	1153	TGGATCATCAGGTGCCATCTGGGATCTGTGTGCTCAACTTCATCTTTTATCAAC	1212						
Qy	673	ATCATCCGGGTGCTTGGCACTTAAGCTTCGGGAGACCAATGCGGCGGTGTGACACAGG	732						
Db	1213	ATCATCCGGGTGCTTGGCACTTAAGCTTCGGGAGACCAATGCGGCGGTGTGACACAGG	1272						
Qy	733	CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTCTGTCGCGCTCTTTGGTGTGAC	792						
Db	1273	CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTCTGTCGCGCTCTTTGGTGTGAC	1332						
Qy	793	TACACGCTTTCATGGCTTGGCTTACACCGAGTCTCAGGACATTTGTGGCAGATCCAG	852						
Db	1333	TACACGCTTTCATGGCTTGGCTTACACCGAGTCTCAGGACATTTGTGGCAGATCCAG	1392						
Qy	853	ATGCATTATGATGCTCTTCAACTCTCTCCAGGATTTTGTGGCATCATATCTGT	912						
Db	1393	ATGCATTATGATGCTCTTCAACTCTCTCCAGGATTTTGTGGCATCATATCTGT	1452						
Qy	913	TTCTGCAATGTGTAGGTGCAGGACAGATTTAGGAAGTCATGAGCCGCTGGACACTGGCG	972						
Db	1453	TTCTGCAATGTGTAGGTGCAGGACAGATTTAGGAAGTCATGAGCCGCTGGACACTGGCG	1512						
Qy	973	TTGACATTCAGCGCAAGACGAAAGTGGAGTAGCAGCTACAGCTATGGCCCAATGGTG	1032						
Db	1513	TTGACATTCAGCGCAAGACGAAAGTGGAGTAGCAGCTACAGCTATGGCCCAATGGTG	1572						
Qy	1033	TCTCAGCAGGTGTGACCAATGTGGCCCCCGTGCAGGACTCAGCCTCCCTCAGCCCC	1092						
Db	1573	TCTCAGCAGGTGTGACCAATGTGGCCCCCGTGCAGGACTCAGCCTCCCTCAGCCCC	1632						
Qy	1093	CGCCTGCTCTGCTCCTACCAATGGCCACTCCAGAGTGTGCTGCGCATGCAAGCCAGGG	1152						
Db	1633	CGCCTGCTCTGCTCCTACCAATGGCCACTCCAGAGTGTGCTGCGCATGCAAGCCAGGG	1692						

Qy	1153	GCTCCAGCCACTGAGACTGAAACCCCTACAGTCACTATATGCGGTTCCCAAGGACGATGGA	1212						
Db	1693	GCTCCAGCCACTGAGACTGAAACCCCTACAGTCACTATATGCGGTTCCCAAGGACGATGGA	1752						
Qy	1213	TTCTTTAAACGGCTCTCTGCTCAGGCTTGGATGAGAGGCTTCCGGGTCTGCGCGCGCCT	1272						
Db	1753	TTCTTTAAACGGCTCTCTGCTCAGGCTTGGATGAGAGGCTTCCGGGTCTGCGCGCGCCT	1812						
Qy	1273	CAATTGTTGAGGAAGATGGGAAACAGTCATGTGATGGGCACTAGG	1320						
Db	1813	CAATTGTTGAGGAAGATGGGAAACAGTCATGTGATGGGCACTAGG	1860						

RESULT 2

US-10-152-319A-1741
; Sequence 1741, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castie, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1741
; LENGTH: 2065
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_020073
US-10-152-319A-1741

Query Match 94.1%; Score 1241.6; DB 18; Length 2065; Best Local Similarity 99.7%; Pred. No. 0; Matches 1244; Conservative 0; Mismatches 4; Indels 0; Gaps 0;									
Qy	73	CTGAGGATATTGACCGCCTAGGCAATGATCTACACCGTGGGATCTCATGTCTCTCGCC	132						
Db	613	CGGAGGATATTGACCGCCTAGGCAATGATCTACACCGTGGGATCTCATGTCTCTCGCC	672						
Qy	133	TCCTCAGCGTGGCTGTGCTCATCTCGGCTATTATTTAGGCGGCTGCACTGCACGCGCAAC	192						
Db	673	TCCTCAGCGTGGCTGTGCTCATCTCGGCTATTATTTAGGCGGCTGCACTGCACGCGCAAC	732						
Qy	193	TACATCCACATGCACATGTTCTCTGCTGTCGCGCGCGGAGCATCTTTCTGTGAAG	252						

1141	ATCATCGGGTGTCTTGCCA	CTAAGCTTTCGGGAGACCAAT	TCGGGGCCGGTGTGACAC	CGG	1200
733	CAGCAGTACCGGAAGCTGCT	CAGGTCACAGCTTGGTGTCT	CGTGGCCGCTCTTTGGTGTGCAC		792
1201	CAGCAGTACCGGAAGCTGCT	CAGGTCACAGCTTGGTGTCT	CGTGGCCGCTCTTTGGTGTCCAC		1260
793	TACACCGCTTTCATGGCTT	TGCCGTACACCGAGGCTCT	CAGGGAACAATTTGGCAGATCCAG		852
1261	TACACCGCTTTCATGGCTT	TGCCGTACACCGAGGCTCT	CAGGGAACAATTTGGCAGATCCAG		1320
853	ATGCATTTACGATGCTCTT	CACTCCTCCAGGATTTTTT	TGTGGCATCATATACTGT		912
1321	ATGCATTTACGATGCTCTT	CACTCCTCCAGGATTTTTT	TGTGGCATCATATACTGT		1380
913	TTCTGCAATGGTGCAGGT	GCAGGACAGATTTAGGAAGT	CATGGAGCCGCTGGACACTGGCG		972
1381	TTCTGCAATGGTGCAGGT	GCAGGACAGATTTAGGAAGT	CATGGAGCCGCTGGACACTGGCG		1440
973	TTGGACTTCAAGCGCAAA	GACCGAAGTGGAGTAGCAGCT	ATAGCCCAATGGTG		1032
1441	TTGGACTTCAAGCGCAAA	GACCGAAGTGGAGTAGCAGCT	ATAGCCCAATGGTG		1500
1033	TCTCACACGAGTGTACCA	ATGTGGGCCCGCTGCAGGACT	TCAGCCTTCCCCCTCAGCCCC		1092
1501	TCTCACACGAGTGTACCA	ATGTGGGCCCGCTGCAGGACT	TCAGCCTTCCCCCTCAGCCCC		1560
1093	CGCTGCTCCTGCTACCT	TACCAATGGCCACTTCC	CAGCTGCTGCCCATGCAAGCCAGGG		1152
1561	CGCTGCTCCTGCTACCT	TACCAATGGCCACTTCC	CAGCTGCTGCCCATGCAAGCCAGGG		1620
1153	GCTCCAGCCACTGAGACT	GTAAACCTTACCAGTCACT	ATATGGCGTTTCCCAAGGACGATGGA		1212
1621	GCTCCAGCCACTGAGACT	GTAAACCTTACCAGTCACT	ATATGGCGTTTCCCAAGGACGATGGA		1680
1213	TTCTCTAA	CGGCTCCTGCTCAGGCT	TCGATGAGGAGGCCCTCCGGGTCT	CGCGCGCGCGCCT	1272
1681	TTCTCTAA	CGGCTCCTGCTCAGGCT	TCGATGAGGAGGCCCTCCGGGTCT	CGCGCGCGCCT	1740
1273	CCATTGTTGCAGGAAGGAT	TGGAAACAGTCA	TGTGA		1308
1741	CCATTGTTGCAGGAAGGAT	TGGAAACAGTCA	TGTGA		1776

RESULT 4

```

US-09-943-446-4
; Sequence 4, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Mus Musculus
; US-09-943-446-4

```

Query Match 86.8%; Score 1146.4; DB 9; Length 1776;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 1180; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 73 CTGAGGATATTTGACCGCTAGGCATGATTCACACGTGGGATACTCCATGTCTCTGCC 132

Query Match		73.2%;	Score 966.8;	DB 15;	Length 1948;		
Best Local Similarity		86.6%;	Pred. No. 3.4e-285;				
Matches 1090;		Conservative	0;	Mismatches 162;	Indels 6;	Gaps 2;	
Qy	69	TGCGCTGGAGGTATTTGACCGCTTAGCATGATCTACACGCTGGGATCTCCATGCTCT	128				
Db	565	TGAACGGGAGGTGTTGACCGCTGGGCATGATTTACACGCTGGCTACTCCGTGTCCT	624				
Qy	129	CGCTTCCTCACGCTGCTGCTCATCTCTGGCTATTTTAGGGGCTGCACTGCACGG	188				
Db	625	GGCTTCCTCACGCTGCTGCTCATCTCTGGCTATTTTAGGGGCTGCACTGCACGG	684				
Qy	189	CAACTACATCACATGACATGTTCTCTGCTTTATGCTGCGCGCCGAGCACTTTCGT	248				
Db	685	CAACTACATCACATGACATGTTCTCTGCTTTATGCTGCGCGCCGAGCACTTTCGT	744				
Qy	249	GAAGGACGCTGTCTACTCTGCTTTCAGCTGGATGAGGCGGAGCGCTTCAAGAGGA	308				
Db	745	CAAGGACGCTGTCTACTCTGCGCCACGCTTGATGAGGCTGAGGCGCTCACCGAGGA	804				
Qy	309	AGAGTTGCACATCATCGCGAGGTGCCACTCCCGCGCGCTGCGCGCTAGCTACGC	368				
Db	805	GGAGCTGCGGCGCATCGCCGAGCGCGCCCGCGCGCTGCCACCGCGCTCCCGGCTACGC	864				
Qy	369	TGCTGCGCGCTGGCGGTGACCTTCTCTACTCTGCTTCTGCTTACCACTACTTGGAT	428				
Db	865	GGCTGCGCGGTGCTGACCTTCTCTACTCTGCTTCTGCTTACCACTACTTGGAT	924				
Qy	429	CCTGGTGGAGGGCTGTAATTGACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGAA	488				
Db	925	TCTGGTGGAGGGCTGTAATTGACAGCCTCATCTTCATGGCCCTTCTCAGAGAAGAA	984				
Qy	489	GTACTGTGGGGCTTACACATCTTTGGCTGGGTCTACCGGCTCTTCGTGGCTGTGTG	548				
Db	985	GTACTGTGGGGCTTACACATCTTTGGCTGGGTCTACCGGCTCTTCGTGGCTGTGTG	1044				
Qy	549	GGTGGGTGTCAGACCACTTTGGCCAACTGGGTGCTGGATCTGAGCTCCGGGCACAA	608				
Db	1045	GGTCAGTGTGACAGCTACCTTGGCCAACTGGGTGCTGGATCTGAGCTCCGGGCACAA	1104				
Qy	609	GAAGTGGATCATCAGGTGCCATCTTGGATCTGTTGCTCAACTTCACTTTTAT	668				
Db	1105	AAAGTGGATCATCAGGTGCCATCTTGGATCTGTTGCTCAACTTCACTTTTAT	1164				
Qy	669	CAACATCATCGGGTGTCTGCACTAGCTTCGGGACCACTGCGGGCGGTGTGACAC	728				
Db	1165	CAATATCGTGGGTGTCTGCGCCAACTGCGGAGCACTGCGGGCGGTGTGACAC	1224				
Qy	729	CAGGACAGGTACCGGAGCTGCTCAGTCCACGTTGGTGTCTGCGCGCTCTTTGGGT	788				
Db	1225	ACGGACAGGTACCGGAGCTGCTCAGTCCACGTTGGTGTCTGCGCGCTCTTTGGGT	1284				
Qy	789	GCACTACACCGTCTTCATGGCTTTGCCGTACACCGAGGTCTCAGGAGCATTTGGGAGAT	848				
Db	1285	CCACTACATTGCTTCATGGCCACACCATACACCGAGGTCTCAGGAGCGCTCTGGCAAGT	1344				
Qy	849	CCAGATGATATGAGATGCTTCACTCTTCAGGGATTTTGTGGCATCATATA	908				
Db	1345	CCAGATGATATGAGATGCTTCACTCTTCAGGGATTTTGTGGCATCATATA	1404				
Qy	909	CTGTTTCTGCAATGCTGAGGTGAGGAGGATGAGGAGTTCATGGAGCGCTGGACACT	968				
Db	1405	CTGTTTCTGCAATGCTGAGGTGAGGAGGATGAGGAGTTCATGGAGCGCTGGACACT	1464				
Qy	969	GGCGTTGAGCTTCAAGCGCAAGACGAGGTGGAGTAGCAGCTACAGCTATGCGCCAAAT	1028				
Db	1465	GGCACTGGAATCTCAAGCGCAAGACGAGGTGGAGTAGCAGCTACAGCTATGCGCCCAAT	1524				
Qy	1029	GGTGTCTCACAGAGTGTACCAATGTGGCGCCCGGTGCGAGGACTCAGGCTCCCGCTCAG	1088				
Db	1525	GGTGTCCACAAAGTGTGACCAATGTGGCGCCCGGTGCGAGGACTCAGGCTCCCGCTCAG	1584				
Qy	1089	CCCCCGC---CTGGCTCTCGCCACTACCAATGGCCACTCCCGAGCTGCTGGCCATGCCAA	1145				

RESULT 7

US-10-305-720-1253
; Sequence 1253, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1253
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g190721
US-10-305-720-1253

Query Match		73.2%;	Score 966.8;	DB 17;	Length 1948;		
Best Local Similarity		86.6%;	Pred. No. 3.4e-285;				
Matches 1090;		Conservative	0;	Mismatches 162;	Indels 6;	Gaps 2;	
Qy	69	TGCGCTGGAGGTATTTGACCGCTTAGCATGATCTACACGCTGGGATCTCCATGCTCT	128				
Db	565	TGAACGGGAGGTGTTGACCGCTGGGCATGATTTACACGCTGGCTACTCCGTGTCCT	624				
Qy	129	CGCTTCCTCACGCTGCTGCTCATCTCTGGCTATTTTAGGGGCTGCACTGCACGG	188				
Db	625	GGCTTCCTCACGCTGCTGCTCATCTCTGGCTATTTTAGGGGCTGCACTGCACGG	684				
Qy	189	CAACTACATCACATGACATGTTCTCTGCTTATGCTGCGCGCCGAGCACTTTCGT	248				
Db	685	CAACTACATCACATGACATGTTCTCTGCTTATGCTGCGCGCCGAGCACTTTCGT	744				
Qy	249	GAAGGACGCTGTCTACTCTGCTTTCAGCTGGATGAGGCGGAGCGCTCACAGAGGA	308				
Db	745	CAAGGACGCTGTCTACTCTGCGCCACGCTTGATGAGGCTGAGGCGCTCACCGAGGA	804				
Qy	309	AGAGTTGCACATCATCGCGAGGTGCCACTCCCGCGCGCTGCGCGCTAGCTACGC	368				
Db	805	GGAGCTGCGGCGCATCGCCGAGCGCGCCCGCGCGCTGCCACCGCGCTCCCGGCTACGC	864				
Qy	369	TGCTGCGCGCTGGCGGTGACCTTCTCTACTCTGCTTCTGCTTACCACTACTTGGAT	428				
Db	865	GGCTGCGCGGTGCTGACCTTCTCTACTCTGCTTCTGCTTACCACTACTTGGAT	924				
Qy	429	CCTGGTGGAGGGCTGTAATTGACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGAA	488				
Db	925	TCTGGTGGAGGGCTGTAATTGACAGCCTCATCTTCATGGCCCTTCTCAGAGAAGAA	984				
Qy	489	GTACTGTGGGGCTTACACATCTTTGGCTGGGTCTACCGGCTGTCTTCGTGGCTGTGTG	548				


```
FILE REFERENCE: 00786/071005
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 08/471,494
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 2010
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (28)...(1806)
US-10-267-730-4

Query Match      73.1%; Score 965.2; DB 16; Length 2010;
Best Local Similarity 86.6%; Pred. No. 1.1e-284;
Matches 1089; Conservative 0; Mismatches 163; Indels 6; Gaps 2;

Qy 69 TGGCTGGAGGTATTTGACCGCTTAGGCATGATCTACACCGTGGGATCTCCATGTCTCT 128
Db 564 TGAACGGAGGTGTTTACCGCTTGGCATGATTTACACCGTGGGCTACTCCGTGTCCT 623

Qy 129 GCGCTCCCTCAGGTGGCTGTCTCATCTGCGCTATTTTAGCGGCTGCACTGCACGG 188
Db 624 GCGCTCCCTCAGGTGGCTGTCTCATCTGCGCTATTTTAGCGGCTGCACTGCACGG 683

Qy 189 CAATCATCATCATGATGATGTTCTGCTGTTTATGCTGCGCGCGGAGCATCTTCGT 248
Db 684 CAATCATCATCATGATGATGTTCTGCTGTTTATGCTGCGCGCGGAGCATCTTCGT 743

Qy 249 GAAGGAGCGCTGTCTACTCTGCTTTCAGCTGGATGAGCGCGCTTCCACAGAGGA 308
Db 744 CAAGGAGCGCTGTCTACTCTGCGCCACCGCTTGTATGAGGCTGAGCGCTTCCACAGAGGA 803

Qy 309 AGAGTTGACATCATCGCGAGGTGCGCACTTCGCGCGCGCGCTGCGCGGTAGGCTACGC 368
Db 804 GGAGCTGCGCGCATCGCGAGGTGCGCACTTCGCGCGCGCGCTGCGCGGTAGGCTACGC 863

Qy 369 TGGCTGCGCGGTGCGCGTACCTTCTCTCTACTCTCTGCTTACCTGCTACCACTACTCTGAT 428
Db 864 GGGCTGAGGGGTGCTGACCTTCTCTCTCTACTCTCTGCTTACCTGCTACCACTACTCTGAT 923

Qy 429 CCTGGTGGAGGGGTGCTACTTTCAGCAGCTCATCTTCATGCGCTTCTTCTCAGAGAGAA 488
Db 924 TCTGGTGGAGGGGTGCTACTTTCAGCAGCTCATCTTCATGCGCTTCTTCTCAGAGAGAA 983

Qy 489 GTACCTGCGGGCTTCAACATCTTTTGGCTGGGTCTACCGGCTGCTTCGTTGGCTGTGTG 548
Db 984 GTACCTGCGGGCTTCAACATCTTTTGGCTGGGTCTACCGGCTGCTTCGTTGGCTGTGTG 1043

Qy 549 GGTGGTGTGAGAGCAACCTTGGCCACACTGGGTGCTGGATCTGAGCTCCGGGCAAA 608
Db 1044 GGTGGTGTGAGAGCAACCTTGGCCACACTGGGTGCTGGATCTGAGCTCCGGGCAAA 1103

Qy 609 GAAGTGGATCATCAGGTGCGCATCTTCGCTGCTGCTCAACTTCACTCTTTTAT 668
Db 1104 AAGTGGATCATCAGGTGCGCATCTTCGCTGCTGCTCAACTTCACTCTTTTAT 1163

Qy 669 CAACATCATCCGGTGTCTGCTCACTAAGCTTCGGGAGACCAATGCGGCGCGGTGTGAC 728
Db 1164 CAATATCGTCCGGTGTCTGCTCACTAAGCTTCGGGAGACCAATGCGGCGCGGTGTGAC 1223

Qy 729 CAGGACAGTACCGGAGCTGCTCAGGTGCACTGGTGTGCTGCTGCGCTCTTTGTTGT 788
Db 1224 ACAGGACAGTACCGGAGCTGCTCAATCCAGCTGGTGTGCTGCTGCGCTCTTTGCGGT 1283

Qy 789 GCATCATACCGCTTTCATGGCTTTCGCTGCTCAGCGAGCTTCTCAGGAGCATTTGTTGG 848
Db 1284 CCATCATATTTCTTCATGGCTTTCGCTGCTCAGCGAGCTTCTCAGGAGCATTTGTTGG 1343

Qy 849 CCAGATGATATATGAGATGCTTTCATCTCCTTCCAGGGATTTTTTTGTTGCCATCATATA 908
```

```
Db 1344 CCAGATGATATATGAGATGCTTTCATCTCTTCCAGGGATTTTTTGTGCAATCATATA 1403
Qy 909 CTGTTTCTGCAATGCTGAGGTGCGAGGAGAGTATAGGAAGTCTAGGAGCGCTGCACT 968
Db 1404 CTGTTTCTGCAATGCGGAGGTACAAGCTGAGATCAAGAAATCTTGGAGCGCTGCACT 1463
Qy 969 GCGTGTGAGACTTCAAGCGCAAGCAAGCAAGTGGAGTAGCAGCTACAGCTATAGTCCCAAT 1028
Db 1464 GGCACCTGAGACTTCAAGCGCAAGCAAGCAAGTGGAGTAGCAGCTATAGTACGCGCCAT 1523
Qy 1029 GGTGTCTCAGCAGGTGAGCAATGTTGGCGCGCGCTGAGGAGTCAAGCTTCCCGCTCAG 1088
Db 1524 GGTGTCTCAGCAGGTGAGCAATGTTGGCGCGCGCTGAGGAGTCAAGCTTCCCGCTCAG 1583
Qy 1089 CCGCGCG-CTGCTCTCTGCTACTACCAATGCGCACTTCCAGCTGCTGCGCAATGCCAA 1145
Db 1584 CCGCGCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1643
Qy 1146 GCCAGGGGCTCCAGCGCACTGAGAC---TGAAACCTTACCACTGCTGCTGCTGCTGCTGCTGCT 1202
Db 1644 GCCAGGGGCTCCAGCGCACTGAGAC---TGAAACCTTACCACTGCTGCTGCTGCTGCTGCTGCT 1703
Qy 1203 GGAGCATGAGTTCCTTAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
Db 1704 GGAGCATGAGTTCCTTAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1763
Qy 1263 GCGCGCGCTTCCATGTTGTCAGGAAGTGGGAAAGTGGGAAAGTGGGAAAGTGGGAAAGTGGG 1320
Db 1764 GCGCGCGCTTCCATGTTGTCAGGAAGTGGGAAAGTGGGAAAGTGGGAAAGTGGGAAAGTGGG 1821
```

RESULT 11

```
US-10-723-860-1005
Sequence 1005, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1005
LENGTH: 2171
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-1005
```

```
Query Match      73.1%; Score 965.2; DB 20; Length 2171;
Best Local Similarity 86.6%; Pred. No. 1.1e-284;
Matches 1089; Conservative 0; Mismatches 163; Indels 6; Gaps 2;

Qy 69 TGGCTGGAGGTATTTGACCGCTTAGGCATGATCTACACCGTGGGATCTCCATGTCTCT 128
Db 755 TGAACGGAGGTGTTTACCGCTTGGCATGATTTACACCGTGGGCTACTCCGTGTCCT 814

Qy 129 GCGCTCCCTCAGGTGGCTGTGCTCATCTGCTGCTATTTTAGCGGCTGCACTGCACGG 188
Db 815 GCGCTCCCTCAGGTGGCTGTGCTCATCTGCTGCTATTTTAGCGGCTGCACTGCACGG 874

Qy 189 CAATCATCATCATGATGATGTTCTGCTGCTTATGCTGCGCGCGGAGCATTTTGT 248
Db 875 CAATCATCATCATGATGATGTTCTGCTGCTTATGCTGCGCGCGGAGCATTTTGT 934

Qy 249 GAAGGAGCGTGTGCTTCTCTGCTGCTTACGCTTACGCTTGGATGAGCGCGAGCGCTTCCAGAGGA 308
```


Db 1197 ACGGACGAGTACCGGAAGCTGCTCAAAATCCCCGCTGGTGTCTATGCCCCCTCTTTGGCGT 1256
Qy 789 GCACTACACCGCTTTTCATGGCTTGGCGTACACCGAGGTCTCAGGAGACATTTGTGGCAGAT 848
Db 1257 CCACATATTGCTTTTCATGGCCACACCATACACCGAGGTCTCAGGAGCGCTCTGGCAAGT 1316
Qy 849 CCAGATGATATGAGATGCTTTCACACTCTTCCAGGGAATTTTGTGGCATCATATA 908
Db 1317 CCAGATGCACTATGAGATGCTTTCACACTCTTCCAGGGAATTTTGTGGCAATCATATA 1376
Qy 909 CTGTTTCTGCAATGGTGGAGTGCAGGAGAGATTTAGGAAGTCAAGGAGCGCTGGACACT 968
Db 1377 CTGTTTCTGCAATGGAGGTACAGCTGAGATCAAGAAATCTTGGAGCGCTGGACACT 1436
Qy 969 GCGCTGGACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGSCCAAT 1028
Db 1437 GGCACCTGACTTCAAGCGAAGGACGAGCGGAGCAGCAGCTATAGCTACGSCCCAT 1496
Qy 1029 GGTGCTCACACGAGTGTACCAATGTGGGCCCCCGTGCAGGACTCAGCCTCCCCCTCAG 1088
Db 1497 GGTGTCCACAAAGTGTGACCAATGTGGGCCCCCGTGTGGGACTCGGCGCTGCCCTCAG 1556
Qy 1089 CCCCCGCG---CTGCTCTCTGCACTACCAATGGCCACTCCAGCTGCTGGCCATGCCAA 1145
Db 1557 CCCCCGCTACTGCGCCACTGCCACCAACACCGGCCACCCCTCAGCTGCTGGCCATGCCAA 1616
Qy 1146 GCCAGGGGCTCCAGCCACTGAGAC---TGAAACCTTACCAGTCACTATGGCGGTCCCAA 1202
Db 1617 GCCAGGGACCCAGCCCTGGAGACCTCGAGACCACACCCACTGCGCATGGCTGCCAA 1676
Qy 1203 GGACGATGATTCCTTAACGGCTCCTGCTCAGGCTCGAGTGGAGAGCGCTCGGCGTCTGC 1262
Db 1677 GGACGATGGGTTCCTCAACGGCTCCTGCTCAGGCTCGAGCGAGGAGGCTCTGGGCGTGA 1736
Qy 1263 GCGGCGCCCTCCATGTTGCGAGGAGGATGGAAACAGTCACTGTGA 1308
Db 1737 GCGGCGCCCTGCTTACAGGAAGAGTGGGAGACAGTCACTGTGA 1782

RESULT 13
US-10-925-095-562
; Sequence 562, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 562
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-925-095-562

Query Match 72.7%; Score 959.6; DB 21; Length 1782;
Best Local Similarity 86.8%; Pred. No. 5.2e-283;
Matches 1081; Conservative 0; Mismatches 159; Indels 6; Gaps 2;
Qy 69 TGGCGTGGAGTATTTGACCGCCCTAGGATGATCTACCGTGGGATCTCCATGTCTCT 128
Db 537 TGAACGGGAGTGTTTGACCGCCCTGGGATGATTTTACACCGTGGGCTACTCCGTGCTCCT 596

Qy 129 CGCTCCCTCACCGTGGCTGTGCTCATCTCTGGCTATTTTAGCGGTGTCACTGCACGCG 188
Db 597 GCGCTCCCTCACCGTGTGTGCTCATCTCTGGCTACTTTTAGCGGTGTCACTGCACGCG 656
Qy 189 CAATACATCCACATGACATGTTCTGTGCTTTATGCTGGCGCGCGGAGCATCTTCGT 248
Db 657 CAATACATCCACATGACATGTTCTGTGCTTTATGCTGGCGCGCGGAGCATCTTCGT 716
Qy 249 GAAGGAGCGCTGTGCTTACTCTCTGGCTTTCAGCTGGATGAGCGCGGCTTCACAGAGGA 308
Db 717 CAAGGAGCGCTGTGCTTACTCTCTGGCGCACGCTTGATGAGGCTGAGCGCTTCACCGAGGA 776
Qy 309 AGAGTTGCAATCATCGCGCAGGTGCCACTCTCGCGCGCGCGCTGCGCGGTAGGCTACGC 368
Db 777 GAGCTGCGCGCATCGCCCGAGCGCGCGCGCTGCGCACCGCGCTGCGCGCTACGC 836
Qy 369 TGCTGCGCGGTGGCGGTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 428
Db 837 GGGCTGCGAGGTGGCTGTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 896
Qy 429 CTGTGTGGAGGGGCTGTACTTGCACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAGAA 488
Db 897 TCTGTGGAGGGGCTGTACTTGCACAGCCTCATCTTCATGGCCCTTCTCTCAGAGAGAA 956
Qy 489 GTACCTGTGGGGTTCACCATCTTGTGGCTGGGTCTACCGGCTGTCTTCGTGGCTGTGTG 548
Db 957 GTACCTGTGGGGTTCACAGTCTTGGGTGGGTCTGCCCGCTGTCTTCGTGGCTGTGTG 1016
Qy 549 GGTGGGTGTGAGAACACCTTGGCCACACTTGGGTGCTGGGATCTGAGCTCGGGGACAA 608
Db 1017 GGTGAGTGTGAGAGTACCTTGGCCAAACACCGGTGCTGGGACTTGGAGCTCGGGGAA 1076
Qy 609 GAAGTGTGATCATCAGGTGCCCATCTGTGGCATCTGTGTGCTCAACTTCATCTCTTTTAT 668
Db 1077 AAGTGTGATCATCAGGTGCCCATCTGTGGCTCCATTTGTGCTCAACTTCATCTCTTCAT 1136
Qy 669 CAATCATCTCCGGTGTCTGCCACTAAGCTTCGGGAGACCAATGCGGCGCGGTGTGACAC 728
Db 1137 CAATATCGTCCGGGTGCTGCCACCAAGCTCGGGAGACCAACGCGCGCGGTGTGACAC 1196
Qy 729 CAGGACGAGTACCGGAGTGTGCTCAGGTCCAGTGGTGTCTGCTGGGCTCTTTGGTGT 788
Db 1197 ACGGACGAGTACCGGAGTGTGCTCAAAATCCCCTGGTGTCTCATGCCCCCTCTTTGGCGT 1256
Qy 789 GCACTACACCGTCTCATGCGCTTGCCTACACCGAGGTCTCAGGAGACATTTGTGGCAGAT 848
Db 1257 CCACTACATTTGCTTCTATGCGCCACACATACACGAGGTCTCAGGAGCGCTCTGGCAAGT 1316
Qy 849 CCAGATGCAATTTAGAGATGCTTTCAACTCTTCCAGGGAATTTTGTGGCATCATATA 908
Db 1317 CCAGATGCACTATGAGATGCTTTCAACTCTTCCAGGGAATTTTGTGGCAATCATATA 1376
Qy 909 CTGTTTCTGCAATGGTGGAGTGCAGGAGAGATTTAGGAAGTCAAGGAGCGCTGGACACT 968
Db 1377 CTGTTTCTGCAATGGGAGGTACAGCTGAGTCAAGAAATCTTGGAGCGCGTGGACACT 1436
Qy 969 GCGTTTGGACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGSCCAAT 1028
Db 1437 GGCACCTGGACTTCAAGCGAAGGACACGAGCGGAGCAGCAGTATAGCTACGSCCCAT 1496
Qy 1029 GGTGTCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCCTCCCCCTCAG 1088
Db 1497 GGTGTCCACACAAAGTGTGACCAATGTCCGCCCCCGTGTGGGACTCGGCGCTGCCCTCAG 1556
Qy 1089 CCCCCGCG---CTGCTCTCTGCACTACCAATGGCCACTCCAGCTGCTGGCCATGCCAA 1145
Db 1557 CCCCCGCTACTGCGCCACTGCCACCAACACCGGCCACCCCTCAGCTGCTGGCCATGCCAA 1616
Qy 1146 GCCAGGGGCTCCAGCCACTGAGAC---TGAAACCTTACCAGTCACTATGGCGGTCCCAA 1202
Db 1617 GCCAGGGACCCAGCCCTGGAGACCTTCGAGACCAACACCCACTGCGCATGGCTGCCAA 1676

QY	1203	GGAGAGATGGATTCCTTAAACGGCTCTCTCTCAGGCCTGGATGAGAGAGCCCTCCGGGTCTGC	1262
Db	1677	GGACGATGGGTTTCTCTCAACGGCTCTCTCTCAGGCCTGGAAGAGAGCCCTCTGGGCCCTGA	1736
QY	1263	CGCGCCGCCCTCCATTGTTGCGAAGGATGGGAAACAGTCATGTGA	1308
Db	1737	CGCGCCACCTGCCCTCGCTACAGGAAGAGTGGGACACAGTCATGTGA	1782

RESULT 14

```

US-10-505-486-14
; Sequence 14, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 14
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Human
US-10-505-486-14

```

Query Match	72.6%	Score 958.2;	DB 21;	Length 1779;
Best Local Similarity	86.8%	Pred. NO. 1.4e-282;		
Matches 1079; Conservative	0;	Mismatches 158;	Indels 6;	Gaps 2;

Qy	69	TGGCTGGAGGTATTGACCGCTAGGCATGATCTACACGTTGGGATACTCCATGTCTCT	128
Db	537	TGAACGGGAGGTGTTTGACCGCTGGGCATGATTTACACGTTGGGCTACTCCGTGTCCCT	596
Qy	129	CGCTCCCTCACGGTGGCTGTGCTCATCTCGGCCTATTTTAGGCGGGCTGCACTGCACGCG	188
Db	597	GGCGTCCCTCACCGTAGCTGTGCTCATCTGGCCCTACTTTAGGCGGCTGCACTGCACGCG	656
Qy	189	CAACTACATCCACATGCACATGTTTCTGTGCTTTATGTCGCGCCGCGAGCACTTTCGT	248
Db	657	CAACTACATCCACATGCACCTGTTTCTGTCTTTCATGCTGCGCGCCGTGAGCATCTTCGT	716
Qy	249	GAAGGACGCTGTGCTTACTCTCTGCTTTCAGCTGGATGAGCCGAGCGCCTCACAGAGGA	308
Db	717	CAAGGACGCTGTGCTTACTCTGCGCGCACGCTTGATGAGGCTGAGCGCCTCACCGAGGA	776
Qy	309	AGATTGCACATCATTCGCGGAGGTGCCACTTCGCGCGCGCTGCGCGCGTAGCTACGC	368
Db	777	GGAGCTCGCGGCCATCGCCAGGCGCCCGCGCCTGCCACCGCCGCTGCGCGCTACGC	836
Qy	369	TGGCTCGCGGTGGCGGTGACCTTCTTCTCTACTTCTGCTACCAACTACTACTGGAT	428
Db	837	GGGCTGAGGGTGGCTGTGACCTTCTCTTTTACTTCTGCGCACCAACTACTACTGGAT	896
Qy	429	CCTGGTGGAGGGGTGTACTTTGCA CAGCCTCATCTTCATGCGCTTTTCTCAGAGAGAA	488
Db	897	TCCTGGTGGAGGGGTGTACTCTGCACAGCCTCATCTTCATGSCCTTCTTCTCAGAGAGAA	956
Qy	489	GTACTGTGGGGCTTCCACATCTTTGGTGGGGTCTACCGGCTGTCTTGTGGGCTGTGTG	548
Db	957	GTACTGTGGGGCTTCCAGTCTTTGGTGGGGTCTGCGCCGCTGTCTTGTGGGCTGTGTG	1016
Qy	549	GGTCGGTGT CAGAGCAACCTTGGCCACACTGGGTGCTGGGATCTGAGCTCCGGGSCAA	608
Db	1017	GGTCAGTGT CAGAGCTACCTTGGCCACACCGGGTGTGGGACTTGAGCTCCGGGAAACA	1076
Qy	609	GAAGTGGATCATTCAGGTGCCATCTCTGGCATCTGTGTGTGCTCAACTTTCATCTTTTAT	668

[illegible]

RESULT 15

```

US-09-943-446-1
; Sequence 1, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891ACPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2177
; TYPE: DNA
; ORGANISM: Canine
US-09-943-446-1
Query Match 68.3%; Score 902.2; DB 9; Length 2177;

```


[illegible]

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 23:04:09 ; Search time 4770 Seconds
(without alignments)
10533.509 Million cell updates/sec

Title: US-09-869-565-1

Perfect score: 1320

Sequence: 1 atgggggcccgcggatcgc.....tcattgtactgggcaactagg 1320

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_ges1:*

9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	844.4	64.0	2090	3	BC031578 Homo sapi
2	839.8	63.6	2009	3	CR595263 full-leng
3	816.8	61.9	1701	9	AY398834 Mus muscu
4	762.6	57.8	929	6	CB183774 AGENCOURT
5	732	55.5	905	4	BG972488 602841263
6	714.2	54.1	876	4	BI102266 602885578
7	703.2	53.3	1037	5	BX381740 BX381740
8	674.8	51.1	1707	9	AY398832 Homo sapi
9	661.4	50.1	808	7	CK595861 AGENCOURT
10	657.4	49.8	838	7	CK598594 AGENCOURT
11	657.4	49.8	1035	5	BQ072459 AGENCOURT
12	650	49.2	949	2	BF789775 602105326
13	642.6	48.7	751	6	CB600301 AGENCOURT
14	629.8	47.7	710	6	CA945951 UI-R-F50-
15	622.2	47.1	765	4	BG970555 602838475
16	613.8	46.5	667	1	AA575668 v64c30.1
17	603	45.7	927	6	CB181376 AGENCOURT
18	595.8	45.1	1051	7	CK231618 ILLUMIGEN
19	591.2	44.8	767	7	CO569702 AGENCOURT
20	581.8	44.1	827	1	AA987157 uc81a02.x
21	581.6	44.1	944	6	CB203544 AGENCOURT
22	576.8	43.7	713	6	CB322650 UI-R-DY0-
23	576.8	43.7	739	7	CK474354 AGENCOURT
24	568.2	43.0	897	2	BF780184 602103870

C	25	546.6	41.4	553	2	BE101119
C	26	529	40.1	653	5	BQ191730 UI-R-BJ1-
C	27	522.8	39.6	701	1	AI327170 mg54d06.x
C	28	519.4	39.3	638	6	CA508167 UI-R-F50-
C	29	512.2	38.8	517	1	AI409036 EST237327
C	30	511.8	38.8	539	5	BQ552052 H4013B06-
C	31	508.8	38.5	662	6	CA508789 UI-R-F50-
C	32	502.4	38.1	1647	2	BF782971 602109056
C	33	496.2	37.6	808	7	CV078279 AGENCOURT
C	34	486	36.8	952	4	BG828526 602752641
C	35	456.8	34.6	556	2	BE749381 200271 MA
C	36	456.8	34.6	1707	9	AY398833 Pan trogl
C	37	447	33.9	898	5	BQ219643 60105084
C	38	444	33.6	456	2	BE115534 UI-R-BJ1-
C	39	442.4	33.5	540	2	BE749383 200299 MA
C	40	439.6	33.3	542	2	BE014986 126918 MA
C	41	436.4	33.1	554	1	AA240746 mv37a11.x
C	42	436	33.0	786	7	CO959840 AGENCOURT
C	43	432.2	32.7	571	5	BQ190700 UI-R-D20-
C	44	429.6	32.5	763	7	CO893473 BoyGen 21
C	45	429.4	32.5	925	4	BF980406 602288296

ALIGNMENTS

RESULT 1	BC031578	2090 bp	mRNA	linear	HTC 01-APR-2004
LOCUS	BC031578				
DEFINITION	Homo sapiens parathyroid hormone receptor 1, mRNA (cDNA clone IMAGE:5180885), with apparent retained intron.				
ACCESSION	BC031578				
VERSION	BC031578.1	GI:21618747			
KEYWORDS	HTC				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 2090)			
AUTHORS	Klausner, R.D., Collins, F.S., Wagner, L.H., Shennen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.O., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Rabe, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903	(2002)
PUBMED	12477932				
REFERENCE	2	(bases 1 to 2090)			
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NTH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapob@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc.				

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 50 Row: b Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4506270
This clone has the following problem: retained intron.

FEATURES

source

1. 2090
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5180885"
/tissue types="Brain, Lung, Testis, adult, pooled whole"
/clone lib="NIH MGC_115"
/lab host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 64.0%; Score 844.4; DB 3; Length 2090;
Best Local Similarity 82.3%; Pred. No. 9.7e-207;
Matches 1035; Conservative 0; Mismatches 156; Indels 67; Gaps 3;

Qy 69 TGCCTGAGGATTTGACCGCTTAGCATGATCTACACGTTGGGATCTCCATGCTCT 128
Db 740 TGAACGGAGGTGTTGACCGCTGGGATGATTTACACCGTGGGCTACTCCGTGCTCT 799

Qy 129 CGCTCTCCTCAGGTGGCTGTGCTCATCTGGCTATTTAGGGGGTGTGACTGCACGCG 188
Db 800 GGGTTCCTCACCAGTAGTGTGCTCATCTGGCTTCTTAGGGGGTGTGACTGCACGCG 859

Qy 189 CAATACATCCATGACATGTTCTGTCTTATGCTGCGCGCCCGAGCATCTTCGT 248
Db 860 CAATACATCCATGACATGTTCTGTCTTATGCTGCGCGCCCGAGCATCTTCGT 919

Qy 249 GAAGGAGCTGTGCTTACTGTGCTTACGCTGGATGAGCGGCTTCACAGAGA 308
Db 920 CAAGGAGCTGTGCTTACTGTGCGCCGCTTGTGAGGCTGAGCGGCTTCACAGAGA 979

Qy 309 AGAGTTGCACATCATCGGAGGTGCCACCTCCCGCGCGCTGCGCGCTAGGCTACGC 368
Db 980 GGAGCTGGCGCCATCGCCAGGCGCCCGCGCGCTGCGCGCTAGGCTACGC 1039

Qy 369 TGGCTGCGCGTGGCGGTGACCTTCTTCTTACTTCTGCTTACCAACTACTCTGGAT 428
Db 1040 GGGCTGCGAGGTGCTGTGACCTTCTTCTTACTTCTGCGCCACCAACTACTCTGGAT 1099

Qy 429 CTTGTTGAGGGGTGCTTACTGACAGCTCATCTTATGCGCCCTTTCTCAGAGAGAA 488
Db 1100 TCTGTTGAGGGGTGCTTACTGACAGCTCATCTTATGCGCCCTTCTTCTCAGAGAGAA 1159

Qy 489 GTACTGTGGGGCTTACCATCTTGTGGTGGGTCTACCGGCTGCTTGGTGGGTGTGTG 548
Db 1160 GTACTGTGGGGCTTACCATCTTGTGGTGGGTCTACCGGCTGCTTGGTGGGTGTGTG 1189

Qy 549 GGTGCTGTTCAGAGCAACCTTTGGCGCAACCTTGGGTGCTGGGATCTGAGCTCCGGGCAAA 608
Db 1190 -----GGGTGCTGGGATCTGAGCTCCGGGCAAA 1218

Qy 609 GAAGTGGATCATCAGGTGCCATCTCGGATCTGTTGTGCTCAACTTCATCTTTTAT 668
Db 1219 AAAGTGGATCATCAGGTGCCATCTCGGCTCCATTTGTGCTCAACTTCATCTTTTAT 1278

Qy 669 CAACATCATCCGGGTGCTTGCCACTTAAGCTTCGGGAGAGCAACCAATCGCGCGGCTGTGACAC 728

Db 1279 CATATCGTCCGGGTGCTCGCCACCAAGCTCGGGAGACCAACCGCGCGGTGTGACAC 1338

Qy 729 CAGGAGAGTACCGGAAGCTGCTCAGGTCCACAGTTGGTCTCGTGGCGCTCTTTGTGTGT 788
Db 1339 ACGGAGAGTACCGGAAGCTGCTCAAAATCCAGCTGGTCTCATGCGCCCTCTTTGGCGT 1398

Qy 789 GCACTACACCGTCTTCATGCGCTTCCGTACACCGAGGTCTCAGGGACATTTGTGGCAGAT 848
Db 1399 CCATCATATGCTTTCATGCGCCACACCATACCCGAGGTCTCAGGGACGCTCTGGCAAGT 1458

Qy 849 CCAGATGCATTATGAGATGCTCTTCAACTCTCTTCCAGGGATTTTGTGTCATCATATA 908
Db 1459 CCAGATGCATTATGAGATGCTCTTCAACTCTCTTCCAGGGATTTTGTGTCATCATATA 1518

Qy 909 CTGTTCTTGAATGTTGAGGTGAGGAGGATAGGAAGTCAATGAGCGCGCTGGACACT 968
Db 1519 CTGTTCTTGAATGTTGAGGTGAGGATCAAGCTGAGATCAAGAAATCTTGGAGCGCTGGACACT 1578

Qy 969 GCGTTGGACTTCAAGCGCAACGACGAGTGGAGTAGCAGCTACAGCTATGCGCCCAAT 1028
Db 1579 GGCATGAGACTTCAAGCGAAAGGACGACGCGGAGCAGAGCTATAGCTACGCGCCCAT 1638

Qy 1029 GGTGTCTTCAACGAGTGTGACCAATGTGGCGCCCGCTGCGAGGACTCAGCGCTCCCGCTCAG 1088
Db 1639 GGTGTCTTCAACGAGTGTGACCAATGTGGCGCCCGCTGCGAGGACTCAGCGCTCCCGCTCAG 1698

Qy 1089 CCCCCCG---CTGCTCTCTGCCACTACCAATGGCGCACTCCAGCTGCTGGCGCATGCCAA 1145
Db 1699 CCCCCCGCTACTCTCCCACTGCCACCAACGCGCCACCTCAGCTGCTGGCGCATGCCAA 1758

Qy 1146 GCCAGGGCTCCAGGCACTGAGAC---TGAAACCTACCACTCACTATGCGGGTTCCTCAA 1202
Db 1759 GCCAGGACCCCGACCTGAGACCTCTGAGACCAACCACTGCGCATGCTGCTCCCAA 1818

Qy 1203 GGCAGTGTGATTCCTTAAACGGCTCTCTCAGCGCTTGGATGAGGAGGCTCCCGGTCTGC 1262
Db 1819 GGCAGTGTGATTCCTTAAACGGCTCTCTCAGCGCTTGGATGAGGAGGCTCTCCCGGTCTGC 1878

Qy 1263 GCGCGCGCTTCAATGTTGAGGAGGATGGGAAACAGTCACTGCTGAGTGGGCACTAGG 1320
Db 1879 GCGCGCGCTTCAATGTTGAGGAGGATGGGAAACAGTCACTGCTGAGTGGGCACTAGG 1936

RESULT 2

CR595263

LOCUS

DEFINITION

of Homo sapiens (human).

ACCESSION

CR595263

VERSION

CR595263.1

KEYWORDS

HTC; CNSLT_CDNA.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 2099)

AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact: Feng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/>

REFERENCE

2 (bases 1 to 2099)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr)- Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a

```
division of Invitrogen.
FEATURES             Location/Qualifiers
     source           1..2009
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI069Y10"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"

ORIGIN
Query Match       63.6%; Score 839.8; DB 3; Length 2009;
Best Local Similarity 87.4%; Pred. No. 1.5e-205;
Matches 919; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 69 TGCCTGAGGATATTTGACCGCTAGGTCATGATCTACACCGTGGGATACTCCATGCTCT 128
Db |||||
Qy 870 TGAACGGGAGGTGTTGACCGCTGGGATGATTTACACCGTGGGCTACTCCGCTGCTCT 929
Db |||||
Qy 129 CGCTCCCTCACGGTGGCTGCTCATCTCTGGCTATTTAGGCGGCTGCACTGCACGG 188
Db |||||
Qy 930 GCGCTCCCTCACCGTAGCTGCTCATCTGGCTTACTTTAGGCGGCTGCACTGCACGG 989
Db |||||
Qy 189 CAACATACATCCACATGACATGTTCTGCTGCTTTATGCTGCGCGCGGAGCATCTTCGT 248
Db |||||
Qy 990 CAACATACATCCACATGACATGTTCTGCTGCTTTATGCTGCGCGCGGAGCATCTTCGT 1049
Db |||||
Qy 249 GAAGGAGCGTGTGCTTACTCTGCTTACCTGCTGATGAGCGGAGCGCTTCACAGAGGA 308
Db |||||
Qy 1050 CAAGAGCGTGTGCTTACTCTGCGGACGCTGTGAGGTGAGGCGCTTCCACGAGGA 1109
Db |||||
Qy 309 AGAGTTGCACATATCGCGAGTGCCACCTTCGCCCGCGCTGCCCGGCTGAGCTACGC 368
Db |||||
Qy 1110 GGAGCTGCGGCCATCGCCAGGCGCCCGCGCTGCCACCGCGCTGCGCGCTACGC 1169
Db |||||
Qy 369 TGGCTGCGCGTGGCGGTGACCTTCTCTCTACTTCTTGCTGCTACCACTACTACTGAT 428
Db |||||
Qy 1170 GGGCTGCGAGGTGCTGTGACCTTCTCTCTTACTTCTTGCGCCCACTACTACTGGAT 1229
Db |||||
Qy 429 CCTGCTGAGGGGCTGTACTTGCACAGCTCATCTTCATGCGCTTTTCTCAGAGAAGAA 488
Db |||||
Qy 1230 TCTGCTGAGGGGCTGTACTTGCACAGCTCATCTTCATGCGCTTCTCAGAGAAGAA 1289
Db |||||
Qy 489 GTACTCTGCGGCTTACCACTTTTGGCTGGGCTTACCGGCTGCTTCTGCTGGCTGTGTG 548
Db |||||
Qy 1290 GTACTCTGCGGCTTACAGCTTTTGGCTGGGCTTCTGCGGCTGCTTCTGCTGGCTGTG 1349
Db |||||
Qy 549 GGTGCTGTGACAGCACTTGGCGCAACACTGGGTGCTGGATCTGAGCTCCGGGCAAA 608
Db |||||
Qy 1350 GGTGAGTGTACAGCTTACCTGGGCAACACCGGCTGCTGGGCTTGGCTCCGGGAA 1409
Db |||||
Qy 609 GAAGTGATCATCCAGGTGCCATCTTGGCATCTGTTGCTCAACTTTCATCTTTTAT 668
Db |||||
Qy 1410 AAAGTGATCATCAGGTGCCATCTTGGCTCAACTTTCATCTTTTAT 1469
Db |||||
Qy 669 CAACATCATCGGCTGTGCTTGCCTTAAAGTTCGGGAGCAATGCGGCGCGGTGACAC 728
Db |||||
Qy 1470 CAATATCGTCCGGTGTGCTCGCCACCAAGTTCGGGAGCAACACCGCGCGGTGTGACAC 1529
Db |||||
Qy 729 CAGCAGAGTACCGGAGCTGCTCAGTTCAGCTTGGTGTGCTGCTGCGGCTTCTTGTGT 788
Db |||||
Qy 1530 ACGCAGCAGTACCGGAGCTGCTCAATCAACGCTGGTGTGCTCATGCCCTCTTTGGCGT 1589
Db |||||
Qy 789 GCATCATACGCTTTCATGGCTTGGCTGACCGAGGCTCTCAGGAGCATTTGTGCGAGAT 848
Db |||||
Qy 1590 CCATCATATTGCTTTCATGGCCACACCATACCGAGGCTCTCAGGAGGCTCTGCGAAGT 1649
Db |||||
Qy 849 CCAGATGATATGAGATGCTCTTCAACTCTCCAGGAGTTTTTGTGTCATCATATA 908
Db |||||
Qy 1650 CCAGATGATATGAGATGCTCTTCAACTCTCCAGGAGTTTTTGTGTCATCATATA 1709
Db |||||
Qy 909 CTGTTTCTGCAATGGTGTGAGGTGACGAGGAGGATTTAGGAAGTTCATGGAGCGGCTGCACT 968
Db |||||
```

[illegible]

CB183774
LOCUS DEFINITION CB183774 929 bp mRNA linear EST 31-JAN-2003
IMAGE:30244792 5', mRNA sequence.
CB183774
VERSION CB183774.1 GI:28182891
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 929)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM0318 row: d column: 17
High quality sequence start: 2
High quality sequence stop: 590.

FEATURES
source Location/Qualifiers
1..929
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30244792"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_164"
/notes="vector: pCMV-Sport6.1; Site 1: EcoRV; Site 2: NotI;
Non-normalized full-length enriched library from pooled
mouse embryonic limb, maxilla and mandible, day 10.5 and
11.5 (size selected for the 0.5-1 kb fragments) Cloned
directionally, priming method: Oligo-dT. cDNA enrichment:
>1k bp, average insert size 1.8k bp. Priming sequence:
5'-GACTAGTCTTAGTCGCGCGGCCCTTT-3'. Tissue contributed
by, David Rowe. Library constructed by Resgen, Invitrogen
Corp."

ORIGIN
Query Match 57.8%; Score 762.6; DB 6; Length 929;
Best Local Similarity 95.5%; Pred. No. 1.1e-185;
Matches 807; Conservative 0; Mismatches 34; Indels 4; Gaps 2;

Qy 73 CTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCC 132
Db 85 CGGGAGGTATTTGACCGCCTGGGATGATCTACACCGTGGGATATTCATGTCTCTGCC 144

Qy 133 TCCCTCACGGTGGCTGTGCTCATCTGGCCCTATTTTAGCGGGTGCACGCGCAAC 192
Db 145 TCCCTCACCGTGGCTGTGCTCATCTAGCCCTATTTTAGCGGGTGCACGCGCAAC 204

Qy 193 TACATCACATGACATGTTTCTGTGCTTTATGCTGGCGCGCGGAGCATCTTGTGAAG 252
Db 205 TACATCACATGACATGTTTCTGTGCTTTATGCTGGCGCGCGGAGCATCTTGTGAAG 264

Qy 253 GAGCTGTGCTTACTCTGGCTTACGCTCGATGAGCCGAGCGCCTCACAGAGGAAGAG 312
Db 265 GACCTGTGCTTACTCTGGCTTACGCTCGATGAGCCGAGCGCCTCACGAGGAAGAG 324

Qy 313 TTGCACATCATCGCGAGGTGCCACTTCCGCCCGCGCTCCGCCCGGTAGGCTACGCTGGC 372
Db 325 TTGCATATCATCGCGAGGTGCCCTTCCGCCCGCGCTCCGCCCGGTAGGCTACGCTGGC 384

Qy 373 TGCCGCGTGGGGTGACCTTCTTCTTACTTCTTGCTACCACTACTACTGATCTTG 432
Db 385 TGCCGCTGGCGTGACCTTCTTCTTACTTCTTGCTACCACTACTACTGATCTTG 444

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
primer="1st strand cDNA was primed with a NotI-oligo (dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 53.3%; Score 703.2; DB 5; Length 1037;
Best Local Similarity 85.6%; Pred. No. 2.5e-170;
Matches 810; Conservative 5; Mismatches 128; Indels 3; Gaps 3;

```
Qy 174 GCTCACTGACGCGCACTACATCCACATGTCCTGCTGCTTATGCTGCGCGC 233
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1033 GCTCACTGACGCGCACTACATCCACATGTCCTGCTGCTTATGCTGCGCGC 974
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 234 CGCAGCATCTTCCTGAAGCAGCTGTCTACTCTGCTTCACTGCTGATGAGCGCA 293
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 973 CGTGAGCATCTTCCTGAAGCAGCTGTCTACTCT- GSCCAGCTTGATGA-GCTGA 916
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 294 CGCCTCAGAGAAAGATTGCAATCATCGCAGGTCACCTCGCGCGCGCTGC 353
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 915 GCGCTCAGCAGAGGA-CKGCGCGCATCGCGCGCGCGCGCGCTGCACCCG 857
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 354 GCGCTAGGCTACCTGCTGCGCGCTGCGGTGACCTTCTCTCTACTTCTGGCTAC 413
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 856 CCGCTGCGGTACCGCGCTGCGGTGCTGCTGCTTCTCTACTTCTGGCTAC 797
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 414 CAATCTACTGATCTCTGCTGAGGCTGTACTTGCACAGCTCATCTTCTGCTG 473
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 796 CAATCTACTGATCTCTGCTGAGGCTGTACTTGCACAGCTCATCTTCTGCTG 737
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 474 TTCTCAGAGAAAGTACCTGCTGCGCTTACCATCTTTGGCTGGGTCTACCGGCTGT 533
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 736 CTTCTCAGAGAAAGTACCTGCTGCGCTTACCATCTTTGGCTGGGTCTACCGGCTGT 677
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 534 CTTGCTGGCTGTGGGTGCTGAGAGCACTTGGCCACACTGGGTGCTGGGATCT 593
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 676 CTTGCTGGCTGTGGGTGCTGAGAGCACTTGGCCACACTGGGTGCTGGGATCT 617
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 594 GAGCTCCGGGCACAAAGTGGATCATCCAGGTGCCATCTGCGCATCTTGTGCTCAA 653
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 616 GAGCTCCGGGCACAAAGTGGATCATCCAGGTGCCATCTGCGCATCTTGTGCTCAA 557
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 654 CTTCACTCTTTTATCAACATCATCCGGGTGCTTGCACCTAAGCTTCGGAGACCAATGC 713
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 556 CTTCACTCTTTTATCAACATCATCCGGGTGCTTGCACCTAAGCTTCGGAGACCAATGC 497
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 714 GGGCGGTGTGACACAGGAGAGTACCGGAGCTGCTCAGGTCACGTTGCTGCTGT 773
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 496 CGCGCGGTGTGACACAGGAGAGTACCGGAGCTGCTCAGGTCACGTTGCTGCTGT 437
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 774 GCGCTCTTTGGTGTGACACAGGAGAGTACCGGAGCTGCTCAGGTCACGTTGCTGCTGT 833
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 436 GCGCTCTTTGGTGTGACACAGGAGAGTACCGGAGCTGCTCAGGTCACGTTGCTGCTGT 377
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 834 GACATTGTGGCAGATCCAGATGCAATTATGAGTCTCTTCAACTCTCTTCCAGGATTTT 893
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 376 GAGCTCTGGCAAGTCCAGATGCAATTATGAGTCTCTTCAACTCTCTTCCAGGATTTT 317
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 894 TGTGGCATCATATACATCTGTTTCTGCAATGTTGAGTGTGAGCGAGATTAAGAGTATG 953
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 316 TGTGCAATCATATACATCTGTTTCTGCAATGTTGAGTGTGAGCGAGATTAAGAGTATG 257
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 954 GAGCGCTGTGACACTGCGGTGAGCTTCAAGCGCAAGACGAGTGGGATGAGCGACTA 1013
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 256 GAGCGCTGTGACACTGCGGTGAGCTTCAAGCGCAAGACGAGTGGGATGAGCGACTA 197
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1014 CAGCTATGGCCCAATGTTGCTTCAAGAGTGTGACCAATGTTGGGCGCCCGTGCAGGACT 1073
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 196 TAGCTAGGCGCCCAATGTTGCTTCAAGAGTGTGACCAATGTTGGGCGCCCGTGCAGGACT 137
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1074 CAGCTATGGCCCAATGTTGCTTCAAGAGTGTGACCAATGTTGGGCGCCCGTGCAGGACT 1119
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 136 CGGCTGCCCCCTCAGCCCCCGCCTACTGCCCACATGCGCACCACTGC 91

RESULT 8

AY398832

LOCUS

DEFINITION

AY398832

ACCESSION

AY398832

VERSION

AY398832.1

KEYWORDS

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1707)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 1707)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

FEATURES

Location/Qualifiers

1..1707

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>1707

/gene="PTHR1"

/locus_tag="HCM0022"

ORIGIN

Query Match 51.1%; Score 674.8; DB 9; Length 1707;

Best Local Similarity 61.9%; Pred. No. 6e-163;

Matches 771; Conservative 0; Mismatches 469; Indels 6; Gaps 2;

Qy 69 TGGCTGTGAGGTATTTGACCGCTAGGCATGATCTACCGTGGGATCTCCATGTCTCT 128

Db 462 TGAACGNN 521

Qy 129 CGCTCCCTCACGGTGGCTGTCTCATCTCGGCTATTTAGGCGGTGCACTGCACGCG 188

Db 522 NNN 581

Qy 189 CAACTACATCCATGCATGTTCTCTGTCTGTCGCGCGCGCGAGCATCTTCGT 248

Db 582 NNN 641

Qy 249 GAAGGACGTGTCTCTCTCTGCTTACGCTGGATGAGCGCGCTCAGAGGA 308

Db 642 NNN 701

Qy 309 AGATTGCATCATCGCGCAGTGCACCTCCGCGCGCGCTGCCGCTAGCTACGC 368

Db 702 NNN 761

Qy 369 TGGCTCGCGGTGGGTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 428

Db 762 GGGCTGAGGGTGGGTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 821

Qy 429 CTTGGTGGAGGGCTGTACTTGCAAGCCTCATCTTTCATGGCCTTTTCTTCAGAGAAGAA 488

```
|||||
Db 822 TCTGTGGGGGTGTACCTGCACAGCCTCACTTCATGGCCTTCTCTCAGAGAGAA 881
Qy 489 GTACCTGTGGGGTTCACCACTTTTGGCTGGGCTACCGGCTGTCTTCGTGGCTGTGTG 548
Db 882 GTACCTGTGGGGTTCACAGCTTCCTGGCTGGNNNNNNNNNNNNNNNNNNNNNNNN 941
Qy 549 GGTGGTGTGACAGCAACCTTGGCCAACATGGGTGTCTGGATCTGAGCTCCGGGCACAA 608
Db 942 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1001
Qy 609 GAAGTGTATCATCAGGTGCCATCTCTGGCATCTGTTGTCTCAACTTCATCTCTTTTAT 668
Db 1002 AAGTGTATCATCAGGTGCCATCTCTGGCATCTGTTGTCTCAACTTCATCTCTTTCAT 1061
Qy 669 CAACATCATCGGGTGTCTGCCATTAAGCTTCGGGAGACCAATGCGGGCGGTGTGACAC 728
Db 1062 CAATATCGTCCGGTGTCTGCCACCAAGCTCGGGAGACCAACGCGCGGGTGTGACAC 1121
Qy 729 CAGCAGAGTACCGGAAGCTGCTCAGGTCCAGCTTGGTGTCTGTCGGCTCTTTGGTGT 788
Db 1122 ACGCAGCAGTACCGGAAGCTGCTCAATCCAGCTGGTGTCTATGCCCTCTTTGGCGT 1181
Qy 789 GCATCATACCGCTTTCATGGCTTTCGCGTACACCGAGTCTCAGGGACATTTGGGCAGAT 848
Db 1182 CCATCATATGCTTTCATGGCCACACCATACACCGAGTCTCAGGGAGCTCTGGCAAGT 1241
Qy 849 CCAGATCATATGAGATGCTCTTCAACTCTCTCCAGGGATTTTTTGTGCCATCATATA 908
Db 1242 CCAGATGCATATGAGATGCTCTTCAACTCTCTCCAGGGATTTTTTGTGCCATCATATA 1301
Qy 909 CTGTTTCTGCAATGAGTGTGAGGTGAGGAGAGATTAGAAGTCATGGAGCGCTGGACACT 968
Db 1302 CTGTTTCTGCAACGGCGAGGTACAGCTGAGATCAAGAAATCTTGGAGCGCTGGACACT 1361
Qy 969 GGCCTTGGACTTCAAGCGCAAGACCAAGTGGGAGTAGCAGCTACAGCTATGCGCCCAAT 1028
Db 1362 GGCATGAGCTTCAAGCGAAGGACACGAGGGAGCAGCAGCTATAGCTACGCGCCCAT 1421
Qy 1029 GGTGTCTCACAGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCTTCCCGCTCAG 1088
Db 1422 GGTGTCCACACAAGTGTGACCAATGTGCGGCCCGGTGTGGAGTCTCGGCTTCCCGCTCAG 1481
Qy 1089 CCCCCGCTCTGCGCTCTGCACTACCAATGCGCACTCCCGAGTCTGCTGCGCCATGCCAA 1145
Db 1482 CCCCCGCTCTGCGCTCTGCACTACCAATGCGCACTCCCGAGTCTGCTGCGCCATGCCAA 1541
Qy 1146 GCGAGGGCTCCAGCCACTGAGAC---TGAAACCTTACCAGTCACTATGGCGGTCCCAA 1202
Db 1542 GCGAGGAGACCCAGCCCTGAGACCTTCGAGACCAACACCTGCTGCTGCTCCCAA 1601
Qy 1203 GGACATGAGATTCCTTAACCGCTCTCTGCTCAGGCTCGATGAGAGCGCTCCGGGTCTGC 1262
Db 1602 GGACATGAGGTTCCTCAACGGCTCTCTGCTCAGGCTCGAGAGGAGGCTCTGGGCTCTGA 1661
Qy 1263 CGGCGCGCTCCATGTTTCAGGAAGATGGAAGACAGTCAATGTGA 1308
Db 1662 GCGGCCACCTGCCCTGCTACAGGAAGATGGGAGACAGTCAATGTGA 1707
```

```
RESULT 9
CK595861
LOCUS CK595861 808 bp mRNA linear EST 22-JAN-2004
DEFINITION AGENCOURT 17840463 NIH MGC 238 Rattus norvegicus cDNA clone
IMAGE:7133139 5', mRNA sequence.
ACCESSION CK595861
VERSION CK595861.1 GI:41108929
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
```

REFERENCE

1 (bases 1 to 808)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM15036 row: 1 column: 01
High quality sequence stop: 641.

FEATURES

source

1..808
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7133139"
/tissue_type="testis, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_238"
/notes="Organ: testis; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTAGTCTCAGATCCGAGCGCGCCGCTTCTCAGAGAAGT 490
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 1.9 kb. This primary
library is normalized (non-normalized primary library is
NIH MGC 237) and was constructed by Express Genomics
(Frédérick, MD)"

ORIGIN

Query Match	Best Local Similarity	Score	661.4;	DB 7;	Length	808;
Matches	Conservative	0;	Mismatches	7;	Indels	0;
Qy 431	TGCTGGAGGGCTGTACTTGCACAGCCTCATCTCATGGCCTTTTCTCAGAGAAGT	490				
Db 1	TGCTGGAGGGCTGTACTTGCACAGCCTCATCTCATGGCCTTTTCTCAGAGAAGT	60				
Qy 491	ACCTGTGGGGCTTCCACATCTTTGGCTGGGGTCTACCGGCTGTCTCGTGGCTGTGGG	550				
Db 61	ACCTGTGGGGCTTCCACATCTTTGGCTGGGGTCTACCGGCTGTCTCGTGGCTGTGGG	120				
Qy 551	TCGGTGTGACAGCAACCTTTGGCCAAACACTGGGTGTCTGGGATCTGAGCTCCGGGCACAAGA	610				
Db 121	TCGGTGTGACAGCAACCTTTGGCCAAACACTGGGTGTCTGGGATCTGAGCTCCGGGCACAAGA	180				
Qy 611	AGTGGATCATCCAGGTGCCCATCTGGCATCTGTTGTGCTCAACTTCATCTTTTATCA	670				
Db 181	AGTGGATCATCCAGGTGCCCATCTGGCATCTGTTGTGCTCAACTTCATCTTTTATCA	240				
Qy 671	ACATCATCGGGTGTGCGCCTTAAGCTTCGGAGACCAATGCGGGCGGTGTGACACCA	730				
Db 241	ACATCATCGGGTGTGCGCCTTAAGCTTCGGAGACCAATGCGGGCGGTGTGACACCA	300				
Qy 731	GGCAGCAGTACCGGAAGCTGCTCAGGTCCAAGTGTGTGCTGTCGCCCTCTTTGGTGTGC	790				
Db 301	GGCAGCAGTACCGGAAGCTGCTCAGGTCCAAGTGTGTGCTGTCGCCCTCTTTGGTGTGC	360				
Qy 791	ACTACACCGTCTTCATGGCCCTTGCCTACACCCAGGCTCTCAGGACATCTTGGCAGATCC	850				
Db 361	ACTACACCGTCTTCATGGCCCTTGCCTACACCCAGGCTCTCAGGACATCTTGGCAGATCC	420				
Qy 851	AGATGCATTATGAGATGCTCTTCAACTCTCCAGGGAATTTTGTGGCCATCATATPACT	910				

Db 421 AGATGCAATATGAGATGCTCTTCAACTCTTCCAGGAGATTTTGTGCGCATATATACT 480
Qy 911 GTTTCGCAATGCTGAGTGCAGGACAGAGATTAGGAAGTCAATGAGCGCTGGACACTGG 970
Db 481 GTTTCGCAATGCTGAGTGCAGGACAGAGATTAGGAAGTCAATGAGCGCTGGACACTGG 540
Qy 971 CGTTGGACTTCAAGCGCAAGACAGAAAGTGGAGTAGCAGCTACAGCTATGAGCCCAATGG 1030
Db 541 CGTTGGACTTCAAGCGCAAGACAGAAAGTGGAGTAGCAGCTACAGCTATGAGCCCAATGG 600
Qy 1031 TGTCTCACACAGAGTGCACCAATGAGCGCCCGCTGGAGACTCAGCTCCCTCAGCC 1090
Db 601 TGTCTCACACAGAGTGCACCAATGAGCGCCCGCTGGAGACTCAGCTCCCTCAGCC 660
Qy 1091 CCGCCTGCCTC 1102
Db 661 CCGCCTGCCTC 672

RESULT 10
CK598594
LOCUS
DEFINITION ACENSCOURT 17840193 NIH_MGC_238 Rattus norvegicus cDNA clone
IMAGE:7133602 5', mRNA sequence.
CK598594
CK598594.1 GI:41111717
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 838)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLAM15037 row: 0 column: 08
High quality sequence stop: 688.
Location/Qualifiers
1. 838
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7133602"
/tissue_type="testis, pooled"
/lab_host="DH10B TONa"
/clone_lib="NIH_MGC_238"
/notes="Organ: testis; Vector: pExpress-1; Site: 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTGATCTAGTCGAGCGCCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 1.9 kb. This primary
library is normalized (non-normalized primary library is
NIH MGC 237) and was constructed by Express Genomics
(Frédérick, MD)"

FEATURES
source

RESULT 11
BQ072459
LOCUS
DEFINITION BQ072459 1035 bp mRNA linear EST 02-APR-2002
AGENCOURT 688764 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5761637
5', mRNA sequence.
BQ072459
BQ072459.1 GI:19901505
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1035)
NIH-MGC <http://img.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

ORIGIN

Query Match 49.8%; Score 657.4; DB 7; Length 838;
Best Local Similarity 99.7%; Pred. No. 1.6e-158;
Matches 669; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 436 GAGGGGCTGTACTTGCACAGCTCATCTTCAATGSCCTTTTCTCAGAGAAGAGTACTG 495
Db 1 GAGGGGCTGTACTTGCACAGCTCATCTTCAATGSCCTTTTCTCAGAGAAGAGTACTG 60
Qy 496 TGGGGCTTCAACATCTTTTGGCTGGGGTCTACCGGCTGTCTTCTGGGGTGTGGGTGGGT 555
Db 61 TGGGGCTTCAACATCTTTTGGCTGGGGTCTACCGGCTGTCTTCTGGGGTGTGGGTGGGT 120
Qy 556 GTACAGACAACCTTGGCCAACTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 615
Db 121 GTACAGACAACCTTGGCCAACTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 180
Qy 616 ATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTTCATCTTTTATCAACATC 675
Db 181 ATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTTCATCTTTTATCAACATC 240
Qy 676 ATCCGGGTGCTTGCCTAAAGCTTTCGGGAGACCAATCGGGCGGGTGTGACACAGGCGAG 735
Db 241 ATCCGGGTGCTTGCCTAAAGCTTTCGGGAGACCAATCGGGCGGGTGTGACACAGGCGAG 300
Qy 736 CAGTACCGGAAGCTGCTCAGGTGCAAGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 795
Db 301 CAGTACCGGAAGCTGCTCAGGTGCAAGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 360
Qy 796 ACCGTCTTCATGCGCTTGGCGTACACCGAGGTCTCAGGAGCATTTGTCGAGATCCAGATG 855
Db 361 ACCGTCTTCATGCGCTTGGCGTACACCGAGGTCTCAGGAGCATTTGTCGAGATCCAGATG 420
Qy 856 CATTATGAGATGCTCTTCAACTCTTTCAGGAGATTTTGTGTCATCATATCTGTTTC 915
Db 421 CATTATGAGATGCTCTTCAACTCTTTCAGGAGATTTTGTGTCATCATATCTGTTTC 480
Qy 916 TGCATGCTGAGTGCAGGCGAGAGATTAGGAAGTATGAGAGCGCTGAGACTGGCGGTG 975
Db 481 TGCATGCTGAGTGCAGGCGAGAGATTAGGAAGTATGAGAGCGCTGAGACTGGCGGTG 540
Qy 976 GACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGCCCCCAATGGTGTCT 1035
Db 541 GACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGCCCCCAATGGTGTCT 600
Qy 1036 CACACGAGTGTGACCAATGTGGCGCCCGCTGCGAGCTCAGCTCCCTCAGCCCCCGC 1095
Db 601 CACACGAGTGTGACCAATGTGGCGCCCGCTGCGAGCTCAGCTCCCTCAGCCCCCGC 659
Qy 1096 CTGCTCTCTGC 1106
Db 660 CTGCTCTCTGC 670

Qy	170	GGCGGCTGCACTGCAAGCGCAACTACATCCACATGCACAT-GTTCTGTGCTTTATGCTG	228
Db	1	GGCGGCTGCACTGCAAGCGCAACTACATCCACATGCACATGCTGCTGTTATGCTG	60
Qy	229	CGCGCGGAGCATCTTCGTGAAGACGCTGCTCTACTCTGGCTTACGCTGATGAG	288
Db	61	CGCGCGGAGCATCTTCGTGAAGACGCTGCTCTACTCTGGCTTACGCTGATGAG	120
Qy	289	GCCGAGCGCCTCACAGAGGAAGTGTGCATCATCGCGAGGTGCCACTCGCGCGCC	348
Db	121	GCCGAGCGCCTCACAGAGGAAGTGTGCATCATCGCGAGGTGCCACTCGCGCC	180
Qy	349	GCTGCGCGGTAGGCTACGCTGGCTGCGCGTGGCGGTGAACCTTCCTCTACTTCTG	408
Db	181	GCTGCGCGGTAGGCTACGCTGGCTGCGCGTGGCTGTGACCTTCTTCCTACTTCTG	240
Qy	409	GCTACCAACTACTACTGATCCTGTGTGGGGCTGTACTTCCACAGCTCATCTTCATG	468
Db	241	GCTACCAACTACTACTGATCTTGGTGGAGGACTGTACTTACACAGCCTCATCTTCATG	300
Qy	469	GCTTTTTTCTCAGAGAAGATGACCTGTGGGGCTTCAACCATCTTGGCTGGGGTCTACCG	528
Db	301	GCTTTTTTCTCAGAGAAGATGATCTGTGGGGCTTCAACCATCTTGGCTGGGGTCTGCGC	360
Qy	529	GCTGTCTTCTGGTGTGTGGTTCGGTTCAGAGCAACCTTGGCCAACTCGGTGCTGG	588
Db	361	GCTGTCTTCTGGTGTGTGGTTCGGTTCAGAGCAACCTTGGCCAACTCGGTGCTGG	420
Qy	589	GATCTGAGCTCGGGCAACAAGAAGTGGATCATCCAGGTGCCCATCTCGCATCTGTGTG	648
Db	421	GACCTGAGCTCTGGGCAACAAGAAGTGGATCATCCAGGTGCCCATCTCGCATCTGTGTG	480
Qy	649	CTCAACTTCATCTTTTATCAACATCATTCGGGTGCTTGCCACTAAGCTTCGGAGACC	708
Db	481	CTCAACTTCATCTCTTTATCAACATCATTCGGGTGCTTGCCACTAAGCTTCGGAGACC	540
Qy	709	AATCGGSCCGGTGTGACACAGGACAGATACCGGAAGCTGCTCAGGTCCACGTTGGTG	768
Db	541	AATCGGSCCGGTGTGACACAGGACAGATACCGGAAGCTGCTCAGGTCCACGTTGGTG	600
Qy	769	CTCGTGCCGCTCTTTGGTGTGCATPACACCGTCTTTCATGGCCCTGCCGTACACCGAGTCC	828
Db	601	CTTGTGCCACTCTTCGGTGTCCACTACACCGTCTTTCATGGCCCTGCCGTACAC--GAGTCC	658
Qy	829	TCAGGACATTTGTGACAGATCCAGA---TGCAATTATGATGCTCTTCAACTCTCTCCAG	885
Db	659	TCAGGACACTGTGACAGATCCAGAATGCCCTATTTAGAAATGCTCTTCAACTCTCTCCAG	718
Qy	886	GGATTTTTTGTGCCATCATATACGTGTTCTGCAATGTTGAGTGCAGGACAGATTTAG	945
Db	719	GGATTTTTTGTGCGCTCATATCTCTGGTCTGCACTGGGTGAGCGCGCCAAATTTGAG	778

RESULT 13
CB600301
LOCUS
DEFINITION
CB600301 710 bp mRNA linear EST 03-APR-2003
AGENCOURT 13041423 NIH MGC 176 Mus musculus cDNA clone
IMAGE:30311807 5', mRNA sequence.
CB600301
CB600301.1 GI:29518157
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 710)
NTH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabps-re@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein

```

CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM95 row: 1 column: 24
High quality sequence stop: 636.
Location/Qualifiers
1. 710
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30311807"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_176"
/notes="Organ: kidney; Vector: pDNR-LIB; Site 1: SfII
(ggccattatggcc); Site 2: SfII (ggccgctctggcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AACGAGTGGTATCAACGACAGTGGCCATTACGCCGG-3' and
5'-ATTCTGAGCCGCGGGCGGCATG-DT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH MGC Library."

```

ORIGIN	BROWNSTEIN (WIKI, NR1) / NOCE: CH18 IS A NING-NC DIADYF.									
	Query Match	48.7%	Score 642.6;	DB 6;	Length 710;					
	Best Local Similarity	95.7%	Pred. No. 1e-154;							
	Matches 671;	Conservative 0;	Mismatches 29;	Indels 1;	Gaps 1					
Qy	396	CCTCTACTTCCTGGCTACCAACTACTACTCTGGATCCTCGTGGAGGGCTGTACTTGCACAG	455							
Db	3	CCTCTACTTCCTGGCTACCAACTACTACTCGATTCTGGTGGAGGACTGTACTTTACACAG	62							
Qy	456	CCTCATCTTCATGGCCCTTTTCTCAGAGAGAAGTACTCTGTGGGGCTTCACCATCTTTGG	515							
Db	63	CCTCATCTTCATGGCCCTTTTCTCAGAGAGAAGTATCTGTGGGGCTTCACCATCTTTGG	122							
Qy	516	CTGGGGTCTACCGCTGTCTTCGTGGCTGTGTGGGTGGTGTCTCAGAGCAACCTTTGGCCAA	575							
Db	123	CTGGGGTCTACCGCTGTCTTCGTGGCTGTGTGGGTGGTGTCTCAGAGCAACCTTTGGCCAA	182							
Qy	576	CACCTGGGTCTGGGATCTGAGCTCCGGGCAACAAGCTGGATCATCCAGGTGCCCATCCT	635							
Db	183	CACCTGGGTCTGGGACCTGAGCTCGGGCAACAAGCTGGATCATCCAGGTGCCCATCCT	242							
Qy	636	GGCATCTGTTGTGCTCAACTTCATCTCTTTTATCAACATCATCCGGGTGTTGGCACTAA	695							
Db	243	GGCATCTGTTGTGCTCAACTTCATCTCTTTTATCAACATCATCCGGGTGTTGGCACTAA	302							
Qy	696	GCTTCGGGAGACCAATGCGGGCCGGTGTGACACCGGACGACGTACCGGAGCTGCTCAG	755							
Db	303	GCTTCGGGAGACCAATGCGGGCCGGTGTGACACCGGACGACGTACCGGAGCTGCTCAG	362							
Qy	756	GTCCACGTTGGTGTCTCGTGGCCGTCTTTGGTGTGCATACACCGCTCTTCATGGCTTGGCC	815							
Db	363	GTCCACGTTGGTGTGTGTCACCTCTTCGGTGTCCACTACACCGCTCTTCATGGCTTGGCC	422							
Qy	816	GTACACCGAGGTCTCAGGGACATTTGTGGCAGATCCAGATGCATTTATGAGATGCTCTTCAA	875							
Db	423	GTACACCGAGGTCTCAGGGACATTTGTGGCAGATCCAGATGCATTTATGAGATGCTCTTCAA	482							
Qy	876	CTCCCTCCAGGATTTTTTGTGGCATCATATACTGTCTTCGCAATGGTGAAGTGCAGGC	935							
Db	483	CTCCCTCCAGGATTTTTTGTGGCATCATATACTGTCTTCGCAATGGTGAAGTGCAGGC	542							
Qy	936	AGAGATTAGGAATGTCATGGAGCCGCTGGACACTGGCGTTCGACTTCAAGCGCAAGCACG	995							
Db	543	AGAGATTAGGAATGTCATGGAGCCGCTGGACACTGGCGTTCGACTTCAAGCGTAAAGCACG	602							
Qy	996	AAGTGGGAGTGAAGCTACAGCTATGTGCCCAATGGTGTCTCTCACACGAGTGTGACCAATGT	1055							

```
Db 603 AAGTGGAGTAGCAGCTACAGCTATGCCCCAATGGTGTACCCACGAGTGTGACCAATGT 662
|||||
Qy 1056 -GGGCCCCCGTGAGGAGCTCAGCGCTCCCTCAGCCCCCGC 1095
|||||
Db 663 GGGGCCCCCGTGCAAGAATCAGCGCTTCCCGCTTACCCCCC 703
|||||

RESULT 14
CA945951/c
LOCUS
DEFINITION
  UI-R-FS0-cqp-m-11-0-UI.s1 NCI CGAP_FS0 Rattus norvegicus cDNA clone
  IMAGE:7356565 3', mRNA sequence.
ACCESSION
  CA945951
VERSION
  CA945951.1 GI:27434431
SOURCE
  EST.
ORGANISM
  Rattus norvegicus (Norway rat)
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
REFERENCE
  1 (bases 1 to 751)
  Bonaudo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  8889548
  PUBMED
  COMMENT
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgaps-remail.nih.gov
  Oligo-dt track not found, Not 1 site shown in beginning of sequence
  is likely internal to the message. cDNA Library Preparation: M.B.
  Soares Lab Clone distribution: clones will be available through
  IMAGE (http://image.llnl.gov)
  Seq primer: M13 FORWARD
  PolyA=yes.
  Location/Qualifiers
    1..751
      /organism="Rattus norvegicus"
      /mol_type="mRNA"
      /strain="Sprague-Dawley"
      /db_xref="taxon:10116"
      /clone="IMAGE:7356565"
      /dev_stage="ADULT"
      /lab_host="DH10B (Life Technologies)"
      /clone_lib="NCI CGAP FS0"
      /note="Vector: p7T3D-Pac (Pharmacia) with a modified
      polylinker; Site_1: Not 1; Site_2: Eco RI; UI-R-FS0 is a
      cDNA library constructed from Swam Rat Chondrosarcoma.
      The library was constructed according to Bonaudo, Lennon
      and Soares, Genome Research, 6:791-806, 1996. First strand
      cDNA synthesis was primed with an oligo-dt primer
      containing a Not 1 site. Double stranded cDNA was ligated
      to an EcoR I adaptor, digested with Not 1, and cloned
      directionally into p7T3-Pac vector. The oligonucleotide
      used to prime the synthesis of first-strand cDNA contains
      a library tag sequence that is located between the Not 1
      site and the (dT)18 tail. The sequence tag for this
      library is AGCGCCGAT. The tumor was provided by Dr Jeff
      Stevens from University of Iowa.
      TAG TISSUE=Rat SRC-JWS Cell Line
      TAG LIB=UI-R-FS0
      TAG_SEQ=AGCGCCGAT"

ORIGIN
  Query Match 47.7%; Score 629.8; DB 6; Length 751;
  Best Local Similarity 99.4%; Pred. No. 2.1e-151;
  Matches 631; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  686 TTGCCACTAGCTTCGGGAGACCAATGCGGCCGGTGTGACACCAGGAGTACCGGA 745
  ^
```

```
Db 751 TTGCCACTAGCTTCGAGACCAATGCGGCCGGTGTGACACCAGGAGTACCGGA 692
|||||
Qy 746 AGCTGCTCAGGTCCACAGTTGGTGTCTCGTGGCGCTCTTTGGTGTGACATACACGCTCTTCA 805
|||||
Db 691 AGCTGCTCAGGTCCACAGTTGGTGTCTCGTGGCGCTCTTTGGTGTGACATACACGCTCTTCA 632
|||||
Qy 806 TGGCCCTTGGCGTACACCGAGGCTCTCAGGAGACATTTGGGAGATCCAGATCCAGATCATTTATGAGA 865
|||||
Db 631 TGGCCCTTGGCGTACACCGAGGCTCTCAGAGACATTTGGGAGATCCAGATCCAGATCATTTATGAGA 572
|||||
Qy 866 TGCTCTTTCAACTCTCTTCCAGGGATTTTGTGTCCTCATATATCTGTTTCTGCAATGGTG 925
|||||
Db 571 TGCTCTTTCAACTCTCTTCCAGGGATTTTGTGTCCTCATATATCTGTTTCTGCAATGGTG 512
|||||
Qy 926 AGGTGAGGAGATTTAGGAAGTCTATGAGCGCGCTGACACTGGCGTTGGACTTCAAGC 985
|||||
Db 511 AGGTGAGGAGATTTAGGAAGTCTATGAGCGCGCTGACACTGGCGTTGGACTTCAAGC 452
|||||
Qy 986 GCAAAGCAGCAAGTGGGAGTAGCAGCTACAGCTATGCCCCCAATGGTGTCTCACACGAGTG 1045
|||||
Db 451 GCAAAGCAGCAAGTGGGAGTAGCAGCTACAGCTATGCCCCCAATGGTGTCTCACACGAGTG 392
|||||
Qy 1046 TGACCAATGTGGGCCCCCGTGCGAGGACTCAGCTTCCCTCAGCCCCCGCTGCTCCTG 1105
|||||
Db 391 TGACCAATGTGGGCCCCCGTGCGAGGACTCAGCTTCCCTCAGCCCCCGCTGCTCCTG 332
|||||
Qy 1106 CCACTACCAATGGGCACTCCAGCTGCTGGCCATGCCAAGCCAGGGGCTCCAGCCACTG 1165
|||||
Db 331 CCACTACCAATGGGCACTCCAGCTGCTGGCCATGCCAAGCCAGGGGCTCCAGCCACTG 272
|||||
Qy 1166 AGACTGAACCCCTACCACTGCTGCGGTTCCTCCAGGACGATGATTCCTTAAACGGCT 1225
|||||
Db 271 AGACTGAACCCCTACCACTGCTGCGGTTCCTCCAGGACGATGATTCCTTAAACGGCT 212
|||||
Qy 1226 CTTGCTCAGGCTTGAGTGGAGGAGCCCTCGGGTCTCGCGGCGCGCTCCATTTGTCAGG 1285
|||||
Db 211 CTTGCTCAGGCTTGAGTGGAGGAGCCCTCGGGTCTCGCGGCGCGCTCCATTTGTCAGG 152
|||||
Qy 1286 AAGATGGGAAACAGTCATGTGATGGGCACTAGG 1320
|||||
Db 151 AAGATGGGAAACAGTCATGTGATGGGCACTAGG 117
|||||

RESULT 15
BG970555
LOCUS
DEFINITION
  602838475F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:4972795
  5', mRNA sequence.
ACCESSION
  BG970555
VERSION
  BG970555.1 GI:14358192
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 765)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-remail.nih.gov
  Tissue Procurement: Jeffrey E. Green, M.D.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM10960 Row: e Column: 20
  High quality sequence stop: 741.
  Location/Qualifiers
    1..765
      source
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 02:48:53 ; Search time 84 Seconds
(without alignments)
2002.866 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGARIAPSLALLCCPVLS.....EASGARPPPLQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2283	100.0	435	3 AAB07529	AAB07529 A mutant
2	2264.5	99.2	446	3 AAY96983	AAY96983 Tethered
3	2195	96.1	591	2 AAR92277	AAR92277 Rat bone
4	2195	96.1	591	2 AAW73316	AAW73316 Parathyro
5	2195	96.1	591	8 ADH61247	ADH61247 Rat bone
6	2187	95.8	591	2 AAR27706	AAR27706 Rat bone
7	2187	95.8	591	7 ADE83416	ADE83416 Rat Prote
8	2146	94.0	591	8 ADO29629	ADO29629 Mouse GPC
9	2077.5	91.0	448	3 AAY96986	AAY96986 Human tet
10	2077.5	91.0	435	3 AAY96987	AAY96987 Human tet
11	2076.5	91.0	450	3 AAY96988	AAY96988 Human tet
12	2008	88.0	593	4 AAB71876	AAB71876 Human PTR
13	2008	88.0	593	6 ABP81872	ABP81872 Human par
14	2008	88.0	593	7 ADE83418	ADE83418 Human pro
15	2008	88.0	593	7 ADF70390	ADF70390 Human PTH
16	2008	88.0	593	8 ADO29628	ADO29628 Human GPC
17	2008	88.0	593	8 ADQ18189	ADQ18189 Human sof
18	2008	88.0	593	8 ADQ76825	ADQ76825 Human wil
19	2008	88.0	593	8 ADR47544	ADR47544 Human par
20	2002	87.7	593	2 AAW73317	AAW73317 Human par
21	2002	87.7	593	4 ABB56385	ABB56385 Non-endog
22	2002	87.7	593	8 ADH61248	ADH61248 Human PTH
23	1960	85.9	593	2 AAR92278	AAR92278 Human kid
24	1957	85.7	595	6 ABG73825	ABG73825 Canine pa
25	1862.5	81.6	614	2 AAR27707	AAR27707 Human kid

26	1710	74.9	585	2 AAR27705	AAR27705 Opossum k
27	1710	74.9	585	2 AAR92276	AAR92276 Opossum k
28	1710	74.9	585	2 AAW73315	AAW73315 Parathyro
29	1710	74.9	585	8 ADH61246	ADH61246 Opossum k
30	1698	74.4	964	7 ADC86169	ADC86169 Human GPC
31	1696	74.3	324	3 AAY96985	AAY96985 Tethered
32	1677.5	73.5	335	3 AAY96984	AAY96984 Tethered
33	1551	67.9	515	2 AAR92275	AAR92275 Opossum k
34	1551	67.9	515	2 AAW73314	AAW73314 Parathyro
35	1551	67.9	515	8 ADH61245	ADH61245 Opossum k
36	1538	67.4	515	2 AAR27704	AAR27704 Opossum k
37	1478	64.7	975	8 ADQ76835	ADQ76835 Parathyro
38	1465	64.2	536	3 AAY90230	AAY90230 Zebrafish
39	1465	64.2	536	3 AAY99600	AAY99600 Zebrafish
40	1465	64.2	536	7 ADC42305	ADC42305 Zebrafish
41	1465	64.2	536	7 ADH61059	ADH61059 Zebrafish
42	1151	50.4	542	3 AAY99601	AAY99601 Zebrafish
43	1130	49.5	542	7 ADC42307	ADC42307 Zebrafish
44	1130	49.5	542	7 ADH61061	ADH61061 Zebrafish
45	1122	49.1	523	3 AAY90231	AAY90231 Zebrafish

ALIGNMENTS

RESULT 1
AAB07529
ID AAB07529 standard; protein; 435 AA.

XX AAB07529;

AC AAB07529;

DT 20-OCT-2000 (first entry)

XX A mutant parathyroid hormone (PTH) receptor designated rdeltaNt.

DE A mutant parathyroid hormone (PTH) receptor designated rdeltaNt.

XX Mutant; parathyroid hormone; PTH; receptor; rdeltaNt;

KW ligand binding domain.

XX Homo sapiens.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

FT Peptide

FT 1..22

FT /note= "signal peptide"

FT Protein

FT 23..435

FT /note= "mature protein"

XX WO200040698-A1.

PN 13-JUL-2000.

XX 31-DEC-1998; 98WO-US027862.

XX 31-DEC-1998; 98WO-US027862.

XX (GHEO) GEN HOSPITAL CORP.

XX Gardella TJ, Kronenberg HM, Potts JT;

XX WPI; 2000-465971/40.

XX N-PSDB; AAA58932.

XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a

XX deletion of the extracellular amino-terminus ligand binding domain,

XX useful in screening assays for identifying agonists and antagonists of

XX PTH receptor activity.

XX Claim 17; Fig 1; Sipp; English.

XX The present sequence represents a mutant parathyroid hormone (PTH)

XX receptor, designated rdeltaNt. The polypeptide is characterised by a

XX deletion of the extracellular amino-terminus ligand binding domain. The

XX receptor has a minimal domain for ligand binding and is, therefore,

XX useful in screening assays designed for the identification of agonists

```
CC and antagonists of PTH receptor activity
XX Sequence 435 AA;
SQ

Query Match 100.0%; Score 2283; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 4e-217;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGAARIAPSLALLCCPVLSAYALVFDRIGMITYTVGYMSLASLTVAVLILAYFRRLH 60
Db 1 MGAARIAPSLALLCCPVLSAYALEVDRIGMITYTVGYMSLASLTVAVLILAYFRRLH 60
Qy 61 CTRNYIHHMFSLPMLRAASIFVKDAVLYSGFTLDEAERLTERELHIIAQVPPPPAAA 120
Db 61 CTRNYIHHMFSLPMLRAASIFVKDAVLYSGFTLDEAERLTERELHIIAQVPPPPAAA 120
Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLGWFTIFGWLPAVF 180
Db 121 GYACRVAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLGWFTIFGWLPAVF 180
Qy 181 AVWGVRAATLANTCWDLSGSHKXWIIQVPIASVVLNFIIRVILATKLRETNAGR 240
Db 181 AVWGVRAATLANTCWDLSGSHKXWIIQVPIASVVLNFIIRVILATKLRETNAGR 240
Qy 241 CDTRQQRKLLRSTLVLPVLFVGHVYTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGPFVA 300
Db 241 CDTRQQRKLLRSTLVLPVLFVGHVYTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGPFVA 300
Qy 301 IIYFCNGEVOAEIRKSWSRWTLALDFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360
Db 301 IIYFCNGEVOAEIRKSWSRWTLALDFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360
Qy 361 PLSRPLPATTNGHSQLPGHAKPGAPATETETLPTVMAVPKDDGFLNGSCGLDEEASGS 420
Db 361 PLSRPLPATTNGHSQLPGHAKPGAPATETETLPTVMAVPKDDGFLNGSCGLDEEASGS 420
Qy 421 ARPPPLLOEGWETVM 435
Db 421 ARPPPLLOEGWETVM 435

RESULT 2
AAY96983
ID AAY96983 standard; protein; 446 AA.
XX AC AAY96983;
XX XX
DT 31-OCT-2000 (first entry)
XX XX
DE Tethered PTH-1 receptor, Tether1.
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
OS Rattus sp.
OS Synthetic.
OS Chimeric.
XX XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT /label= PTH-1_receptor_signal_sequence
FT Peptide 24..32
FT /label= PTH_residues_1-9
FT Peptide 33..36
FT /label= linker
FT Protein 37..446
FT /label= PTH-1_receptor
FT /note= "residue 182 to end"
XX XX
FN WO200039278-A2.
XX XX
XX PD 06-JUL-2000.
XX XX
```

RESULT 3
AAR92277 standard; protein; 591 AA.
XX AC AAR92277;
XX DT 25-MAR-2003 (revised)
XX DT 18-MAY-1996 (first entry)
XX DE Rat bone PTH/PTHrP receptor.
XX KW Parathyroid hormone; receptor; parathormone; PTH;
XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
XX KW hypercalcaemia; hypocalcaemia; cancer.
XX OS Rattus sp.
XX FH Key Location/Qualifiers
XX FT Region 1..192
XX FT Region /label= Extracellular_region
XX FT Region 193..211
XX FT Region /label= Transmembrane_region
XX FT Region 212..221
XX FT Region /label= Intracellular_region
XX FT Region 222..240
XX FT Region /label= Transmembrane_region
XX FT Region 241..299
XX FT Region /label= Extracellular_region
XX FT Region 300..316
XX FT Region /label= Transmembrane_region
XX FT Region 317..325
XX FT Region /label= Intracellular_region
XX FT Region 326..342
XX FT Region /label= Transmembrane_region
XX FT Region 343..364
XX FT Region /label= Extracellular_region
XX FT Region 365..383
XX FT Region /label= Transmembrane_region
XX FT Region 384..408
XX FT Region /label= Intracellular_region
XX FT Region 409..428
XX FT Region /label= Transmembrane_region
XX FT Region 429..444
XX FT Region /label= Intracellular_region
XX FT Region 445..463
XX FT Region /label= Transmembrane_region
XX FT Region 464..591
XX FT Region /label= Intracellular_region
XX PN US5494806-A.
XX PD 27-FEB-1996.
XX PF 06-APR-1992; 92US-00864475.
XX PR 05-APR-1991; 91US-00681702.
XX PA (GEHO) GEN HOSPITAL CORP.
XX PI Potts JT, Juppner H, Segre GV, Schipani E, Kronenberg HM;
XX PI Abou-Samra A;
XX PI WPI; 1996-113028/14.
XX PI N-PSDB; AAT15947.
XX DR DNA encoding vertebrate parathyroid hormone receptor - useful for
XX DR diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia, cancer
XX DR etc.
XX PS Claim 1; Fig 3A-3E; 64pp; English.
XX PS A rat parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)

CC receptor (AAR92277) is encoded by cDNA clone R15B (AAT15947) isolated
CC from a rat osteosarcoma ROS 17/2.8 cDNA library. The receptor a G-protein
CC linked receptor having 7 transmembrane domains. It induces an increase in
CC intracellular cAMP and calcium upon challenge with PTH or PTHrP.
CC Recombinant receptor can be produced in vector/host cell systems and used
CC in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and
CC hypocalcaemia, to screen for (ant)agonists and to raise antibodies. Host
CC cells expressing the receptor are used for diagnostic measurement of PTH
CC serum levels. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 591 AA;
Query Match 96.1%; Score 2195; DB 2; Length 591;
Best Local Similarity 73.6%; Pred. No. 3.2e-208;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSAVAL----- 25
DB 1 MGAARIAPSLALLCCPVLSAVALVDADDVTKERQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
DB 61 NIMESDKGWTTPASTSGKPRKEKAGKFPESKENKDVPTGSRRRGRPCLPENDNIVCWPL 120
QY 26 ----- 25
DB 121 GAPGEVAVVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPVGHNRWTWANYSECLKFMTNRE 180
QY 26 -EVFDRGLGMYTVGYSMASLTVAVLLAYFRRLHCTRNYYIHMHPLSPMLRAASTFVK 84
DB 181 REVFDRLGMYTVGYSMASLTVAVLLAYFRRLHCTRNYYIHMHPLSPMLRAASTFVK 240
QY 85 DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYWIL 144
DB 241 DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGWGLPAVFVAVVWVGVVTRATLANTCWDLSGHHK 204
DB 301 VEGLYLHSLIFMAFFSEKKYLGFTIFGWGLPAVFVAVVWVGVVTRATLANTCWDLSGHHK 360
QY 205 WIIQVPILASVNLNFIINIRVLATKURETNAGRCDTROQYRKLLRSLVLPLFGVH 264
DB 361 WIIQVPILASVNLNFIINIRVLATKURETNAGRCDTROQYRKLLRSLVLPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIQMHEMLFNSFGQFFVAILIYFCNCEVQAEIRKSWRWTLA 324
DB 421 YTVFMALPYTEVSGTLWQIQMHEMLFNSFGQFFVAILIYFCNCEVQAEIRKSWRWTLA 480
QY 325 LDFKPKARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQPLGHAKPG 384
DB 481 LDFKPKARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQPLGHAKPG 540
QY 385 APATETETPLVTMAVPKDDGFLNGSCSLDEERAGSARPPPLLOEGWETVM 435
DB 541 APATETETPLVTMAVPKDDGFLNGSCSLDEERAGSARPPPLLOEGWETVM 591
RESULT 4
AAW73316
ID AAW73316 standard; protein; 591 AA.
XX AC AAW73316;
XX DT 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor R15B.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; rat.
XX OS Rattus sp.
XX PN US5840853-A.

```
XX 24-NOV-1998.
PD 06-JUN-1995; 95US-00471494.
PF 05-APR-1991; 91US-00681702.
XX 06-APR-1992; 92US-00864475.
XX (GEHO ) GEN HOSPITAL CORP.
XX Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;
PI Kronenberg HM;
XX WPI; 1999-034124/03.
XX DR N-PSDB; AAV08390.
XX Antbody to parathyroid hormone receptor - for diagnostic or therapeutic
PT use.
PT
XX Claim 6; Fig 3; 63pp; English.
XX This sequence represents the rat parathyroid hormone (PTH) receptor R15B,
CC which is targeted by the antibody of the invention. The antibody of the
CC invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia
XX SQ Sequence 591 AA;
Query Match 96.1%; Score 2195; DB 2; Length 591;
Best Local Similarity 73.6%; Pred. No. 3.2e-208; Indels 156; Gaps 1;
Matches 435; Conservative 0; Mismatches 0;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTASTGKPKREKASKGFYFESKENKDVPTGSRRRGRPCLPEDWNIVCWPL 120
Qy 26 ----- 25
Db 121 GAGEVAVPCPDYIYDFNKHGHAYRCDRNGSWEVVPGHNRWTWANYSECLKFWTNETRE 180
Qy 26 -EVFDRLGMIYTVGYSMASLTVAVLILAYFRRLHCTRNIIHMHFSLPMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLTVAVLILAYFRRLHCTRNIIHMHFSLPMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEARLLEELHIIAQVPPPPAAAAGYACRVAVTFPLATNYYWIL 144
Db 241 DAVLYSGFTLDEARLLEELHIIAQVPPPPAAAAGYACRVAVTFPLATNYYWIL 300
Qy 145 VEGYLHSLIFMAPFSKKYLMGFTIFGWGLPAVFVAVVGVVATLANTGCWDLSSGHK 204
Db 301 VEGYLHSLIFMAPFSKKYLMGFTIFGWGLPAVFVAVVGVVATLANTGCWDLSSGHK 360
Qy 205 WIIQVPILASVNLFIINIRIATKLRETNAGRCDTTQQYRKLLRSLTLVLPFGVH 264
Db 361 WIIQVPILASVNLFIINIRIATKLRETNAGRCDTTQQYRKLLRSLTLVLPFGVH 420
Qy 265 YTVPMALPYTEVSTLWQIOMHYEMLFNSQGFVAILIYFCNGEVOAEIRKWSRWTLA 324
Db 421 YTVPMALPYTEVSTLWQIOMHYEMLFNSQGFVAILIYFCNGEVOAEIRKWSRWTLA 480
Qy 325 LDFRKARSSSSSYSGPMVSHTSVTNVGPRAGLSPLSLPRLPATTNGHSQLPGHAKPG 384
Db 481 LDFRKARSSSSSYSGPMVSHTSVTNVGPRAGLSPLSLPRLPATTNGHSQLPGHAKPG 540
Qy 385 APATETETLPVTMAVPKDDGFLNGSCSLDEASGSARPPPLIQEGWETVM 435
Db 541 APATETETLPVTMAVPKDDGFLNGSCSLDEASGSARPPPLIQEGWETVM 591
```

```
RESULT 5
ADH61247
ID ADH61247 standard; protein; 591 AA.
XX
XX ADH61247;
XX
XX 25-MAR-2004 (first entry)
XX Rat bone PTH/PTHrP receptor, R15B.
XX osteopathic; Parathyroid hormone receptor; hypercalcaemia;
XX hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
XX oesophagus multiple myeloma; hypocalcaemia; cytostatic; rat; PTH; PTHrP;
XX PTH-related protein; receptor.
XX Rattus rattus.
XX
XX Key Location/Qualifiers
XX Region 133..211
XX /note= "Transmembrane region 1"
XX Region 222..240
XX /note= "Transmembrane region 2"
XX Region 300..316
XX /note= "Transmembrane region 3"
XX Region 326..342
XX /note= "Transmembrane region 4"
XX Region 365..383
XX /note= "Transmembrane region 5"
XX Region 409..428
XX /note= "Transmembrane region 6"
XX Region 445..463
XX /note= "Transmembrane region 7"
XX
XX US2003153041-A1.
XX
XX 14-AUG-2003.
XX
XX 09-OCT-2002; 2002US-00267730.
XX
XX 05-APR-1991; 91US-00681702.
XX 06-APR-1992; 92US-00864475.
XX 06-JUN-1995; 95US-00471494.
XX 24-NOV-1998; 98US-00199874.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX Schipani E;
XX
XX WPI; 2004-051107/05.
XX DR N-PSDB; ADH61258.
XX
XX New isolated DNA encoding parathyroid hormone receptor polypeptides,
XX useful for diagnosing and treating disorders associated with parathyroid
XX hormone receptors, e.g. hypercalcaemia, osteoporosis or multiple myeloma.
XX
XX Disclosure; SEQ ID NO 20; 71pp; English.
XX
XX The invention relates to parathyroid hormone (PTH) receptor and its
XX corresponding nucleic acid sequence. The parathyroid hormone receptor
XX polypeptides, polynucleotides and antibodies are useful for diagnosing,
XX prognosticating and treating disorders associated with parathyroid
XX hormone receptors, e.g. hypercalcaemia, hyperparathyroidism,
XX osteoporosis, carcinomas of the breast, lung and prostate, epidermoid
XX cancers of the head and neck of the oesophagus, multiple myeloma, or
XX hypocalcaemia. The DNAs and polypeptides are also useful for screening
XX candidate compounds for antagonistic or agonistic effects on parathyroid
XX hormone receptor activity. The compounds are also useful in manufacturing
XX diagnostic agents used as diagnostic tools to diagnose hypercalcaemia and
XX to distinguish between hypercalcaemic conditions. The present sequence is
XX rat bone PTH/PTHrP (PTH-related protein) receptor protein.
```


541 APATETETLPVTMAVPKDDGLNGSCSLDEASGSARPPPLLOEGWETVM 591

Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;

RESULT 7

ADE83416
ID ADE83416 standard; protein; 591 AA.

XX AC ADE83416;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P25961, SEQ ID NO 11011.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX XX (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P25961.

XX PT New composition comprising two or more isolated polypeptides, useful for
XX PS preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC Claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
XX CC injury (CCI) and spared nerve injury (SNI)).

XX CC The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 591 AA;

Query Match 95.8%; Score 2187; DB 7; Length 591;
Best Local Similarity 73.4%; Pred. No. 2e-207;

QY 1 MGAARTAPSLALLCCPVLSAVAL----- 25

DB 1 MGAARTAPSLALLCCPVLSAVALDDVFTKEQIFLLHRAQAQCKLLKEVLHTAA 60

QY 26 ----- 25

DB 61 NIMESDKWTPASTSGKPRKEKASGKYPESKENKDVPDTSRRRGRPCLPEDWNIVCWPL 120

QY 26 ----- 25

DB 121 GAGEVAVVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPVGNRTWANYSECLKFTMTNRE 180

QY 26 -EVFDRLGMIYTVGYSMASLTVAVLIILAYFRLHCTRNVIHMHMFLSFMRAASIFVK 84

DB 181 REVFDRLGMIYTVGYSMASLTVAVLIILAYFRLHCTRNVIHMHMFLSFMRAASIFVK 240

QY 85 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAAAGYAGCRVAVTFFLYLATNYYWIL 144

DB 241 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAAAGYAGCRVAVTFFLYLATNYYWIL 300

QY 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGNGLPAVFAVWVGVVRAVTLANTGCDLSSGHKK 204

DB 301 VEGLYLHSLIFMAFFSEKKYLGFTIFGNGLPAVFAVWVGVVRAVTLANTGCDLSSGHKK 360

QY 205 WIIQVPILASVNLFINIIRVLATKLRETNAGRCTRQYRKLLRSTLVLPVFGVH 264

DB 361 WIIQVPILASVNLFINIIRVLATKLRETNAGRCTRQYRKLLRSTLVLPVFGVH 420

QY 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYFCNGEVOAIBKRSWRTLA 324

DB 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYFCNGEVOAIBKRSWRTLA 480

QY 325 LDFKRVARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRPATNGHSQLPGHAKPG 384

DB 481 LDFKRVARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRPATNGHSQLPGHAKPG 540

QY 385 APATETETLPVTMAVPKDDGLNGSCSLDEASGSARPPPLLOEGWETVM 435

DB 541 APATETETLPVTMAVPKDDGLNGSCSLDEASGSARPPPLLOEGWETVM 591

RESULT 8

ADO29629

ID ADO29629 standard; protein; 591 AA.

XX AC ADO29629;

XX DT 29-JUL-2004 (first entry)

XX DE Mouse GPCR PTHR1, SEQ ID NO:731.

XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX KW transgenic mouse; neurological disorder; adrenal gland disorder;
XX KW colon disorder; intestinal disorder; cardiovascular disorder;
XX KW muscular disorder; blood disorder; immune disorder; bone disorder;
XX KW joint disorder; metabolic disorder; nutritive disorder; cancer;
XX KW kidney disorder; liver disorder; lung disorder; breast disorder;
XX KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
XX KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
XX KW thymus disorder; thyroid disorder; antiparkinsonian; antinemic;
XX KW cytostatic; antiinflammatory; vasotropic; antiangiinal; antiarrhythmic;
XX KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
XX KW virucide; hepatocrotropic; antibacterial; antianemic; antiseborrhoeic;
XX KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
XX KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
XX KW murine; receptor.

XX OS Mus musculus.

XX PN WO2004040000-A2.

XX XX


```
DR N-PSDB; AAA51735.
XX
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
XX Example 4; Fig 17; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
XX Sequence 448 AA;
SQ
Query Match 91.0%; Score 2077.5; DB 3; Length 448;
Best Local Similarity 88.8%; Pred. No. 9.8e-197;
Matches 398; Conservative 11; Mismatches 26; Indels 13; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYAL-----EVFDRLGMIYTVGYSMSLASLTVA 49
DB 1 MGTARIAPGLALLCCPVLSSAYAVSEIQLMHGGGGEVFDRLGMIYTVGYSVLSLTVA 60
QY 50 VLILAYPRRLHCTRNYYHMEFLSFMLRAASIFVKDAVLYSGFTLDEAERLTHEELHITA 109
DB 61 VLILAYPRRLHCTRNYYHMEFLSFMLRAVSIKDAVLYSGATLDEAERLTHEELRAIA 120
QY 110 QVPPPPAAAGVAGCVAVTFEFLYFLATNYWILVEGLYHSLIFMAFFSEKKYLWGFT 169
DB 121 QAPPPPPATAAGVAGCVAVTFEFLYFLATNYWILVEGLYHSLIFMAFFSEKKYLWGFT 180
QY 170 IFWGGLPAVFAVWVGVVVRATLANTGCDLSSGHKKWIIQVPILASVVLNFIINIRVL 229
DB 181 VFGGLPAVFAVWVSVRATLANTGCDLSSGNKKWIIQVPILASIVLNFILINIRVL 240
QY 230 ATKLRNAGCDTRQYRKLLRSTLVLPFLGVHYTVFMAIPYTESVSGTLWQIQHYEM 289
DB 241 ATKLRNAGCDTRQYRKLLRSTLVLMPLFGVHYTVFMAIPYTESVSGTLWQIQHYEM 300
QY 290 LFNSFQGFVVAIIYFCNGEVQAEIRKSWSRWTLALDFKPKARSGSSSYSGPMVSHTSV 349
DB 301 LFNSFQGFVVAIIYFCNGEVQAEIRKSWSRWTLALDFKPKARSGSSSYSGPMVSHTSV 360
QY 350 TNGVPRAGLSPLSPR-LPPATNGHSQLPGHAKPGAPATET-ETLPVTMAVPRKDDGFLN 407
DB 361 TNGVPRVGLPLSPRLPPTATNGHSQLPGHAKPGTLETTPPMAAPKDDGFLN 420
QY 408 GSCSGLDEEASGARPPPLQEGWETVM 435
DB 421 GSCSGLDEEASGARPPPLQEEWETVM 448
RESULT 10
AA96987
ID AA96987 standard; protein; 435 AA.
XX
AC AA96987;
XX
XX 31-OCT-2000 (first entry)
DE Human tethered PTH-1 receptor, hdelNT.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
```

```
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX WO200039278-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX DR N-PSDB; AAA51736.
XX
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
XX Example 4; Fig 18; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
XX Sequence 435 AA;
SQ
Query Match 91.0%; Score 2077; DB 3; Length 435;
Best Local Similarity 90.8%; Pred. No. 1.1e-196;
Matches 397; Conservative 10; Mismatches 26; Indels 4; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYALVEFDRLGMIYTVGYSMSLASLTVAIILAYPRRLH 60
DB 1 MGTARIAPGLALLCCPVLSSAY--EVFDRLGMIYTVGYSVLSLTVAIILAYPRRLH 58
QY 61 CTNRYIHMELFSFMLRAASIFVKDAVLYSGFTLDEAERLTHEELHIAQVPPPPAAAV 120
DB 59 CTNRYIHMELFSFMLRAVSIKDAVLYSGATLDEAERLTHEELRAIAQAPPPATAAA 118
QY 121 GYACRCVAVTFEFLYFLATNYWILVEGLYHSLIFMAFFSEKKYLWGFTIFGGLPAV 180
DB 119 GYACRCVAVTFEFLYFLATNYWILVEGLYHSLIFMAFFSEKKYLWGFTVFGGLPAV 178
QY 181 AVWGVVRATLANTGCDLSSGHKKWIIQVPILASVVLNFIINIRVLATKLRETNAGR 240
DB 179 AVWVSVRATLANTGCDLSSGNKKWIIQVPILASIVLNFILINIRVLATKLRETNAGR 238
QY 241 CDTRQYRKLLRSTLVLPFLGVHYTVFMAIPYTESVSGTLWQIQHYEMLFNSFQGFVVA 300
DB 239 CDTRQYRKLLRSTLVLMPLFGVHYTVFMAIPYTESVSGTLWQIQHYEMLFNSFQGFVVA 298
QY 301 ILYCFNGEVQAEIRKSWSRWTLALDFKPKARSGSSSYSGPMVSHTSVTNVPAGLSL 360
DB ILYCFNGEVQAEIRKSWSRWTLALDFKPKARSGSSSYSGPMVSHTSVTNVPAGLSL 360
```


PA (MILL-) MILLENNIUM PHARM INC.
XX Hodge MR, Lloyd C, Weich NS;
XX WPI; 2001-138653/14.
PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.
XX Disclosure; Fig 2; 145pp; English.
PS
XX The present sequence is a human G-protein coupled receptor (GPCR) used
CC for comparison with the seven transmembrane domain of a novel GPCR
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate GPCR expression. Such diseases includes immune,
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR polypeptides
CC in samples
XX
SQ Sequence 593 AA;
Query Match 88.0%; Score 2008; DB 4; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCKRLKVELQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSASTGKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHLCWPL 120
QY 26 ----- 25
Db 121 GAGEVAVPCPDYIDFNHKGHAYRCRDNGSWELVPGHNRWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYIHMHFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRNYIHMHFSLFMLRAVSIFVK 240
QY 85 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTTEELRAIAQAPPPPPATAAGYACRVAVTFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAPFSEKKYLWGFTIRGWGLPAVFVAVVWGVVRATLANTCGWDLSSGHKI 204
Db 301 VEGLYLHSLIFMAPFSEKKYLWGFTIRGWGLPAVFVAVVWGVVRATLANTCGWDLSSGNK 360
QY 205 WIIQVPIASVLNFIILFIIIRVIAKLKRLNAGRCDDTRQQYRKLRLSTLVLPFGVH 264
Db 361 WIIQVPIASVLNFIILFIIIRVIAKLKRLNAGRCDDTRQQYRKLKLSLVLMPLFGVH 420
QY 265 YTVFMAPLYTEVSTLWQIQHYEMLFNSQGFVAILIYCFNGEVOAETKRSWRWTLA 324
Db 421 YIVFMATPYTEVSTLWQVQHYEMLFNSQGFVAILIYCFNGEVOAETKRSWRWTLA 480
QY 325 LDFKRRKSSSSYSYSGPMWHSHTVTVNGVRAGLSPLSPR-LPPATTNGHSGOLPGHAKP 383
Db 481 LDFKRRKSSSSYSYSGPMWHSHTVTVNGVRAGLSPLSPRLPATTNGHSGOLPGHAKP 540
QY 384 GAPATET-ETLPVTMAYPKDDGFLNGSCGLDEEASGARPPPLQLQEWETVM 435
Db 541 GTPALETLETTTPPAWAAAPKDDGFLNGSCGLDEEASGARPPPALQLQEWETVM 593

RESULT 13
ABP81872
XX ID ABP81872 standard; protein; 593 AA.
XX AC ABP81872;
XX DT 04-MAR-2003 (first entry)
XX DE Human parathyroid hormone receptor 1 protein SEQ ID NO:229.
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX OS Homo sapiens.
XX PN WQ200261087-A2.
XX PD 08-AUG-2002.
XX PF 19-DEC-2001; 2001WO-US050107.
XX PR 19-DEC-2000; 2000US-0257144P.
XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX PI Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
XX N-PSDB; AB242719.
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX Disclosure; Fig 1; 523pp; English.
XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnoses. AB242523 to AB242869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention

```
XX SQ Sequence 593 AA;
Query Match      88.0%; Score 2008; DB 6; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSGTSGKPKDKASGLYPESEDEKAPTGSRYGRPCLPEDWHLWCPL 120
Qy 26 ----- 25
Db 121 GAGEVAVPCPDYIDFNHKGHAYRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
Qy 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRYNIHMHFLSFMRLAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRYNIHMHFLSFMRLAASIFVK 240
Qy 85 DAVLYSGFTLDEARLTEEELHIIAQVPPPAAGVAGCRVATSFELFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTEEELRAIAQAPPPATAAGYAGCRVATFPLFLATNYWIL 300
Qy 145 VEGLYLSLIFMAFFSEKKYLWGFTTFGWGLPAVFVAVVWVSVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLSLIFMAFFSEKKYLWGFTTFGWGLPAVFVAVVWVSVRATLANTGCDLSSGNKK 360
Qy 205 WIIQVPILASVLNFIINIRVLATKLRETNAGRCTROQYRKLLKSTLVLMPLFGVH 264
Qy 265 YTVFMALPYTEVSGTLWQIQHYEMLFNSFGQFVAILIYCFNCGEVQAEIRKHSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQVQHYEMLFNSFGQFVAILIYCFNCGEVQAEIRKHSRWTLA 480
Qy 325 LDFPKRKARSGSSSYSGPMWSHTSVTVNGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
Db 481 LDFPKRKARSGSSSYSGPMWSHTSVTVNGPRVGLGLPLSPRLTATTNGHPQLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAVPKODGFLNGSCGLDEBASGARPPPLLBQGWETVM 435
Db 541 GTPALETLETTPMAAPKODGFLNGSCGLDEBASGPERPALLQBEWETVM 593

RESULT 14
AD883418
XX AC ADE883418 standard; protein; 593 AA.
XX AC ADE883418;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein Q03431, SEQ ID NO 11013.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX XX 27-FEB-2003.
XX XX 14-AUG-2002; 2002WO-US025765.
XX XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
```

(GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.

Woelf C, D'urso D, Befort K, Costigan M;
WPI; 2003-268312/26.
GENBANK; Q03431.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 593 AA;

Query Match 88.0%; Score 2008; DB 7; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSGTSGKPKDKASGLYPESEDEKAPTGSRYGRPCLPEDWHLWCPL 120
Qy 26 ----- 25
Db 121 GAGEVAVPCPDYIDFNHKGHAYRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
Qy 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRYNIHMHFLSFMRLAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRYNIHMHFLSFMRLAASIFVK 240
Qy 85 DAVLYSGFTLDEARLTEEELHIIAQVPPPAAGVAGCRVATSFELFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTEEELRAIAQAPPPATAAGYAGCRVATFPLFLATNYWIL 300
Qy 145 VEGLYLSLIFMAFFSEKKYLWGFTTFGWGLPAVFVAVVWVSVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLSLIFMAFFSEKKYLWGFTTFGWGLPAVFVAVVWVSVRATLANTGCDLSSGNKK 360
Qy 205 WIIQVPILASVLNFIINIRVLATKLRETNAGRCTROQYRKLLKSTLVLMPLFGVH 264
Qy 265 YTVFMALPYTEVSGTLWQIQHYEMLFNSFGQFVAILIYCFNCGEVQAEIRKHSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQVQHYEMLFNSFGQFVAILIYCFNCGEVQAEIRKHSRWTLA 480
Qy 325 LDFPKRKARSGSSSYSGPMWSHTSVTVNGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
Db 481 LDFPKRKARSGSSSYSGPMWSHTSVTVNGPRVGLGLPLSPRLTATTNGHPQLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAVPKODGFLNGSCGLDEBASGARPPPLLBQGWETVM 435
Db 541 GTPALETLETTPMAAPKODGFLNGSCGLDEBASGPERPALLQBEWETVM 593

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 05:24:16 ; Search time 27 Seconds
(without alignments)
1202.679 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLIQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	96.1	591	2	US-08-468-249A-20
2	2008	88.0	593	4	US-09-631-603-21
3	2002	87.7	593	2	US-08-468-249A-21
4	2002	87.7	593	4	US-09-826-509-563
5	1710	74.9	595	1	US-08-142-439A-6
6	1710	74.9	585	2	US-08-142-551B-125
7	1710	74.9	585	2	US-08-869-477-6
8	1710	74.9	585	2	US-08-468-249A-19
9	1551	67.9	515	2	US-08-468-249A-18
10	1465	64.2	536	4	US-09-449-632-2
11	1130	49.5	542	4	US-09-449-632-4
12	1068	46.8	575	4	US-09-449-632-5
13	1050.5	46.0	550	4	US-09-631-603-20
14	1044.5	45.8	550	4	US-09-826-509-565
15	1036	45.4	541	3	US-08-468-011A-2
16	1036	45.4	541	3	US-09-236-468A-2
17	1036	45.4	541	5	PCT-US95-07085-2
18	960.5	42.1	207	4	US-08-811-519-31
19	776	34.0	459	4	US-09-694-519-4
20	775.5	34.0	1324	2	US-08-811-897A-56
21	775.5	34.0	1324	3	US-09-201-474-56
22	773.5	33.9	444	4	US-09-694-519-6
23	772	33.8	459	4	US-09-694-519-3
24	772	33.8	459	4	US-09-694-519-8
25	762.5	33.4	458	1	US-08-112-817C-2
26	762.5	33.4	458	4	US-09-694-519-5
27	762.5	33.4	458	4	US-09-694-519-7

28	757.5	33.2	449	1	US-08-142-439A-5	Sequence 5, Appli
29	757.5	33.2	449	2	US-08-869-477-5	Sequence 5, Appli
30	752.5	33.0	457	4	US-09-631-603-23	Sequence 23, Appli
31	752.5	33.0	457	4	US-09-694-519-1	Sequence 1, Appli
32	747	32.7	440	4	US-09-631-603-22	Sequence 22, Appli
33	746.5	32.7	457	4	US-09-826-509-579	Sequence 579, App
34	741	32.5	460	4	US-09-694-519-2	Sequence 2, Appli
35	738	32.3	440	4	US-09-826-509-567	Sequence 567, App
36	718	31.4	447	4	US-09-694-519-9	Sequence 9, Appli
37	687	30.1	448	2	US-08-811-897A-22	Sequence 22, Appli
38	687	30.1	448	3	US-08-855-213-22	Sequence 22, Appli
39	687	30.1	448	3	US-09-201-474-22	Sequence 22, Appli
40	687	30.1	468	4	US-09-631-603-19	Sequence 19, Appli
41	687	30.1	525	2	US-08-811-897A-23	Sequence 23, Appli
42	687	30.1	525	2	US-08-855-213-23	Sequence 23, Appli
43	687	30.1	525	3	US-09-201-474-23	Sequence 23, Appli
44	684	30.0	448	2	US-08-811-897A-18	Sequence 18, Appli
45	684	30.0	448	2	US-08-855-213-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-20

Query Match 96.1%; Score 2195; DB 2; Length 591;
Best Local Similarity 73.6%; Pred. No. 1e-209;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

```
QY 1 MGAARTAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARTAPSLALLCCPVLSSAYALVDADDVFTKEBQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTASTSGKPRKEKAGKFPYPSKENKDVPTGSRRRGRPCLPEDWDNICWPL 120
QY 26 ----- 25
Db 121 GAPCEVVAVPCPDYIYDFNKHGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EYFDRLGMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYIHMHFLSMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYIHMHFLSMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEEBELHIIAQVPPPPAAAAAGYAGCRVAVTFPLYFLATNYWIL 144
Db 241 DAVLYSGFTLDEAERLTEEBELHIIAQVPPPPAAAAAGYAGCRVAVTFPLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVVRATLANTGCWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVVRATLANTGCWDLSSGHKK 360
QY 205 WIIQVPIASVNLNFIINIRVLATKLRNAGRCRTQOYRKLLRSTLVLPVLFVGH 264
Db 361 WIIQVPIASVNLNFIINIRVLATKLRNAGRCRTQOYRKLLRSTLVLPVLFVGH 420
QY 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWRWTLA 480
QY 325 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATNNGHSQLPGHAKPG 384
Db 481 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATNNGHSQLPGHAKPG 540
QY 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEASGSRPPPLLOEGWETVM 435
Db 541 APATETETLPTVMAVPKDDGFLNGSCSGLDEASGSRPPPLLOEGWETVM 591
```

RESULT 2

```
US-09-631-603-21
; Sequence 21, Application US/09631603
; Patent No. 6733990
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
; FILE REFERENCE: Secretin-like Family and Uses Thereof
; CURRENT FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-02-29
; PRIOR FILING DATE: 2000-02-29
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-603-21
```

```
Query Match 88.08; Score 2008; DB 4; Length 593;
Best Local Similarity 67.38; Pred. No. 4.3e-191;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARTAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARTAPGLALLCCPVLSSAYALVDADDVMTKEBQIFLLHRAQAQCEKRLKEVLQRP 60
```

```
QY 26 ----- 25
Db 61 SIMESDKGWTASTSGKPRKDKASGKLYPESEBEDKEAPTGSRYRGRPCLPEDWDHILCWPL 120
QY 26 ----- 25
Db 121 GAPCEVVAVPCPDYIYDFNKHGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EYFDRLGMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYIHMHFLSMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYIHMHFLSMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEEBELHIIAQVPPPPAAAAAGYAGCRVAVTFPLYFLATNYWIL 144
Db 241 DAVLYSGFTLDEAERLTEEBELHIIAQVPPPPAAAAAGYAGCRVAVTFPLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVVRATLANTGCWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVVRATLANTGCWDLSSGHKK 360
QY 205 WIIQVPIASVNLNFIINIRVLATKLRNAGRCRTQOYRKLLRSTLVLPVLFVGH 264
Db 361 WIIQVPIASVNLNFIINIRVLATKLRNAGRCRTQOYRKLLRSTLVLPVLFVGH 420
QY 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWRWTLA 480
QY 325 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATNNGHSQLPGHAKP 383
Db 481 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATNNGHSQLPGHAKP 540
QY 384 GAPATET-ETLPTVMAVPKDDGFLNGSCSGLDEASGSRPPPLLOEGWETVM 435
Db 541 GTPALETETLPTVMAVPKDDGFLNGSCSGLDEASGSRPPPALOEWETVM 593

RESULT 3
US-08-468-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-249A-21

Query Match 87.7%; Score 2002; DB 2; Length 593;
Best Local Similarity 67.1%; Pred. No. 1.7e-190;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
DB 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLORPA 60
QY 26 ----- 25
DB 61 SIMESDKGWTASSTGKPKDKASGLYPSEEDKEAPTGSRYGRPCLPEDWDHILCWPL 120
QY 26 ----- 25
DB 121 GAGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
QY 26 -EYFDRGLMIYTVGYSMASLSTAVLILAYFRRLHCTRYNIHMHMFLSFMRLRAASIFVK 84
DB 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRYNIHMHMFLSFMRLRAVSIFVK 240
QY 85 DAVLYSGFTLDEARLTEELHIIAQVPPPPAAAGYACRVAVTFFLYFLATNYTWIL 144
DB 241 DAVLYSGATLDEARLTEELRAIAQAPPPATAAGYACRVAVTFFLYFLATNYTWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGTFIIGWGLPAVFAVAVVGVVRATLANTCGWDLSSGHKK 204
DB 301 VEGLYLHSLIFMAFFSEKKYLWGTFVFGWGLPAVFAVAVVSVRATLANTCGWDLSSGNKK 360
QY 205 WIQVPIASVNLNFIINIRVLATKLRETNAGRCDTTQQYRKLRLSTLVLVPLFGVH 264
DB 361 WIQVPIASVNLNFIINIRVLATKLRETNAGRCDTTQQYRKLRLSTLVLVPLFGVH 420
QY 265 YTVFMALPYTEVSGTLQIQHYEMLFNSFGQFFVAIIYCFNGEVOAEIKKSWSRWTLA 324
DB 421 YIVFMATPYTEVSGTLQIQHYEMLFNSFGQFFVAIIYCFNGEVOAEIKKSWSRWTLA 480
QY 325 LDFKRRKARSSSSYSYGPVMSHTSVTNVGPVAGLSPLSPR-LPPATTNGHSQLPGHAKP 383
DB 481 LDFKRRKARSSSSYSYGPVMSHTSVTNVGPVAGLSPLSPR-LPPATTNGHSQLPGHAKP 540
QY 384 GAPATET-ETLPTVMAVPKDDGFLNGSCGLDEASGARPPPLLOEGWETVM 435
DB 541 GTPALETLETPPAMAAPKDDGFLNGSCGLDEASGARPPPLLOEGWETVM 593

RESULT 4

US-09-826-509-563
Sequence 563, Application US/09826509
Patent No. 6806054
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826.509
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 09/170,496
PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 563
LENGTH: 593
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 87.7%; Score 2002; DB 4; Length 593;
Best Local Similarity 67.1%; Pred. No. 1.7e-190;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
DB 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLORPA 60
QY 26 ----- 25
DB 61 SIMESDKGWTASSTGKPKDKASGLYPSEEDKEAPTGSRYGRPCLPEDWDHILCWPL 120
QY 26 ----- 25
DB 121 GAGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
QY 26 -EYFDRGLMIYTVGYSMASLSTAVLILAYFRRLHCTRYNIHMHMFLSFMRLRAASIFVK 84
DB 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRYNIHMHMFLSFMRLRAVSIFVK 240
QY 85 DAVLYSGFTLDEARLTEELHIIAQVPPPPAAAGYACRVAVTFFLYFLATNYTWIL 144
DB 241 DAVLYSGATLDEARLTEELRAIAQAPPPATAAGYACRVAVTFFLYFLATNYTWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGTFIIGWGLPAVFAVAVVGVVRATLANTCGWDLSSGHKK 204
DB 301 VEGLYLHSLIFMAFFSEKKYLWGTFVFGWGLPAVFAVAVVSVRATLANTCGWDLSSGNKK 360
QY 205 WIQVPIASVNLNFIINIRVLATKLRETNAGRCDTTQQYRKLRLSTLVLVPLFGVH 264
DB 361 WIQVPIASVNLNFIINIRVLATKLRETNAGRCDTTQQYRKLRLSTLVLVPLFGVH 420
QY 265 YTVFMALPYTEVSGTLQIQHYEMLFNSFGQFFVAIIYCFNGEVOAEIKKSWSRWTLA 324
DB 421 YIVFMATPYTEVSGTLQIQHYEMLFNSFGQFFVAIIYCFNGEVOAEIKKSWSRWTLA 480
QY 325 LDFKRRKARSSSSYSYGPVMSHTSVTNVGPVAGLSPLSPR-LPPATTNGHSQLPGHAKP 383
DB 481 LDFKRRKARSSSSYSYGPVMSHTSVTNVGPVAGLSPLSPR-LPPATTNGHSQLPGHAKP 540
QY 384 GAPATET-ETLPTVMAVPKDDGFLNGSCGLDEASGARPPPLLOEGWETVM 435
DB 541 GTPALETLETPPAMAAPKDDGFLNGSCGLDEASGARPPPLLOEGWETVM 593

RESULT 5

US-08-142-439A-6
Sequence 6, Application US/08142439A
Patent No. 5670360
GENERAL INFORMATION:
APPLICANT: Thorens, Bernard
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5670360 No. 5670360disk of No. 5670360th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 39,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
; US-08-142-439A-6
```

```
Query Match 74.9%; Score 1710; DB 1; Length 585;
Best Local Similarity 80.2%; Pred. No. 2e-161;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;

QY 26 EVFDRGLMIYTVGYSMASLTAVLILAYFRRLHCTRNVIHMHMFLSFMLRAASIFVKD 85
DB 179 EVFDRGLMIYTVGYSLGSLTAVLILGYFRRLHCTRNVIHMHMFLSVFMLRAVSIFIKD 238

QY 86 AVLYSGTDLDEARLLEEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFYLATNYWILV 145
DB 239 AVLYSGVSTDEIERITEELRAFFE--PPADKA-GFVGCRVAVTVFLYPLTNTYWILV 295

QY 146 EGYLHSLIFMAFFSEKKYLWGFTIIGWGLPAFVAVVWVTRATLANTCGWDLSSGHKKW 205
DB 296 EGYLHSLIFMAFFSEKKYLWGFTLFGWGLPAFVAVVWVTRATLANTCGWDLSSGNKKW 355

QY 206 IIQVPILASVVLNFIPIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLVPLFGVHY 265
DB 356 IIQVPILAAIVNFIPIINIRVLATKLRETNAGRCDTROQYRKLLKSTLVLVPLFGVHY 415

QY 266 TVFMALPYTEVSGTLWQIQMHYEMFLNSFGFFVAIIYFCNCEVQAEIRKKSWSRWTLAL 325
DB 416 IVFMATPYTEVSGTLWQVQMHYEMFLNSFGFFVAIIYFCNCEVQAEIRKKSWSRWTLAL 475

QY 326 DFKKRKARSGSSSYSGPMVSHTSVTNNGPRAGLSPLSLPRLPP--ATTNGHSOLPGHAK 382
DB 476 DFKKRKARSGSSTSYSGPMVSHTSVTNNGPRGGLALSPLSLPRLAPGAGASANGHHQLPGYVK 535

QY 383 PGAPATETETLPVTMAVP--KDDGFLNGSCSGLDEEASGSGARPPPLIQEWETVM 435
DB 536 HG--SISENSLPSPGPEPGTKDDGYLNG--SLGYEPMVGE-QPPPLLEBERETVM 585
```

RESULT 6

```
US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
```

```
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
; US-08-142-551B-125
```

```
Query Match 74.9%; Score 1710; DB 2; Length 585;
Best Local Similarity 80.2%; Pred. No. 2e-161;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;

QY 26 EVFDRGLMIYTVGYSMASLTAVLILAYFRRLHCTRNVIHMHMFLSFMLRAASIFVKD 85
DB 179 EVFDRGLMIYTVGYSLGSLTAVLILGYFRRLHCTRNVIHMHMFLSVFMLRAVSIFIKD 238

QY 86 AVLYSGTDLDEARLLEEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFYLATNYWILV 145
DB 239 AVLYSGVSTDEIERITEELRAFFE--PPADKA-GFVGCRVAVTVFLYPLTNTYWILV 295

QY 146 EGYLHSLIFMAFFSEKKYLWGFTIIGWGLPAFVAVVWVTRATLANTCGWDLSSGHKKW 205
DB 296 EGYLHSLIFMAFFSEKKYLWGFTLFGWGLPAFVAVVWVTRATLANTCGWDLSSGNKKW 355

QY 206 IIQVPILASVVLNFIPIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLVPLFGVHY 265
DB 356 IIQVPILAAIVNFIPIINIRVLATKLRETNAGRCDTROQYRKLLKSTLVLVPLFGVHY 415

QY 266 TVFMALPYTEVSGTLWQIQMHYEMFLNSFGFFVAIIYFCNCEVQAEIRKKSWSRWTLAL 325
DB 416 IVFMATPYTEVSGTLWQVQMHYEMFLNSFGFFVAIIYFCNCEVQAEIRKKSWSRWTLAL 475

QY 326 DFKKRKARSGSSSYSGPMVSHTSVTNNGPRAGLSPLSLPRLPP--ATTNGHSOLPGHAK 382
DB 476 DFKKRKARSGSSTSYSGPMVSHTSVTNNGPRGGLALSPLSLPRLAPGAGASANGHHQLPGYVK 535
```


Qy 383 PGAPATETETLPTVMAPV--KDDGFLNGSCSLDEEASGSARPPLIQEGWEITVM 435
| : || : | ||||| ||||| | : ||||| : ||||
Dd 536 HG--STSENSLPSSGPPEGTKDDGYING--SGLYEPMWGE-QPPLLEERETVM 585

RESULT 7
US-08-869-477-6
; Sequence 6, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
;

Query Match	74.9%	Score 1710;	DB 2;	Length 585;
Best Local Similarity	80.2%;	Pred. No. 2e-161;		
Matches 333;	Conservative	27;	Mismatches 42;	Indels 13;
				Gaps 7;

Qy	26	EVDRLGMIYTVGYSMISLASLTVAVLILAYFRRLLHCTRNVIHMHMFSLFMLRAASIFVKD	85
		: : : : : : : : :	
Db	179	EVDRLGMIYTVGYGISLSGLSTVAVLILGYFRRLLHCTRNVIHMHLVFVSFMLRAVSIFIKD	238

Qy	86	AVLYSGFTLDEAERITEEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYYTILV	145
		: : : : : : : : :	
Db	239	AVLYSGVSTDEIERITEEELAFTE--PPADKA-GVGGRVAVTVELYFLATNYYTILV	295

Qy 146 EGIYLSLIFMAPSEKKYLGFTTFGWGLPAFVAVVGVPRATLANTGCWDLSSGHKKW 209

Dp 296 EGIYLSLIFMAPSEKKYLGFTTFGWGLPAFVAVVGVPRATLANTGCWDLSSGNKKW 355

206	Qy	IIQVPIIASVVLNPIILPIINIRVLATKLRNAGCDTROQYRKLLRSTLVLVLPFGVHY	265
356	Db	IIQVPIIAATVWNPIILPIINIRVLATKLRNAGCDTROQYRKLLKSTLVLMLPFGVHY	415
266	Qy	TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILYFCNCGEVOAQRKKSWSRWTLAL	325
416	Db	IVFMATPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILYFCNCGEVOAQRKKSWSRWTLAL	475
326	Qy	DFRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRIPLP---ATTNGHSQLPGHAK	382
476	Db	DFRKARSGSSTYSYSGPMVSHTSVTNVGPRGLALSPLPAPGAGASANGHHQLPGYVK	535
383	Qy	PGAPATETETLPVTMAVP--KDGDFLNGSCGLDEEASGARPPPLPQEGWETVM	435
536	Db	HSISENSLPSGPPGPKDKGYLNG--SGLYEPMVGE--OPPLPEEBREBETVM	595

RESULT 8
US-08-468-249A-19
; Sequence 19, Application US/08468249A
; Patent No. 586148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston.
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-19

Query Match	74.9%	Score 1710;	DB 2;	Length 585;
Best Local Similarity	80.2%;	Pred. No. 2e-161;		
Matches 333;	Conservative	27;	Mismatches 42;	Indels 13;
				Gaps 7;

[illegible]

QY 86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 145

Db 239 AVLYSGVSTDEIRITEELRAFT--PPADKA-GFVGCRVAVTVFLYFLATNYIWL 235
Qy 146 EGYLHSLIFMAFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 205
Db 296 EGYLHSLIFMAFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 355
Qy 206 IIQVPILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
Db 356 IIQVPILAAIVNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 415
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 325
Db 416 IVFMATPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 475
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLPRLPP---ATTNGHSQLPQAK 382
Db 476 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLPRLAPCAGASANGHQLPQYK 535
Qy 383 PGAPATETETLPVTMAVP--KDDGFLNGSCSGLDEEASGSRPPPLLOEGWETVM 435
Db 536 HG--SISENSLPSSGPEGTCKDDOYLNG--SGLYEPMVGB-QPPPLLEBERETVM 585

RESULT 9

US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 586148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-18

Query Match 67.9%; Score 1551; DB 2; Length 515;
Best Local Similarity 86.6%; Pred. No. 1.1e-145;
Matches 291; Conservative 16; Mismatches 24; Indels 3; Gaps 2;

Qy 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYIHMHFLSFMLRAASIFVKD 85
Db 179 EVFDRGLMIYTVGYSMSLSGLTAVLILGFRRLHCTRNYIHMHFLFVSPMLRAVSIFIKD 238
Qy 86 AVLYSGFTLDEARLTEREELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYIWL 145
Db 239 AVLYSGVSTDEIRITEELRAFT--PPADKA-GFVGCRVAVTVFLYFLATNYIWL 295
Qy 146 EGYLHSLIFMAFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 205
Db 296 EGYLHSLIFMAFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 355
Qy 206 IIQVPILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
Db 356 IIQVPILAAIVNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 415
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 325
Db 416 IVFMATPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 475
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLP 361
Db 476 DFKRKARSGSSSYSGPMVSHTSVTNVGPRGMPCP 511

RESULT 10
US-09-449-632-2
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 536
; ORGANISM: zebrafish
US-09-449-632-2

Query Match 64.2%; Score 1465; DB 4; Length 536;
Best Local Similarity 68.8%; Pred. No. 4.3e-137;
Matches 284; Conservative 45; Mismatches 66; Indels 18; Gaps 4;

Qy 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYIHMHFLSFMLRAASIFVKD 85
Db 139 EVFDRLIYTVGYSISLSGLSMVATVILGYFRRLHCTRNYIHMHFLSFMLRAISIFVKD 198
Qy 86 AVLYSGFTLDEARLTEREELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYIWL 145
Db 199 VLYSGSALQEMERITVEDKSITEAPP---ANKTOFIGCKVAVTLFLYFLATNYIWL 255
Qy 146 EGYLHSLIFMAFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 205
Db 256 EGYLHSLIFMTFFSDRKYLWGFTLIGWGPAMFVTIWSVRATLADTECDLSAGNLKW 315
Qy 206 IIQVPILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
Db 316 IQVPILTAIVNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 375
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 325
Db 376 IVFMATPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 435
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPPLPATTNGHSQLPQAKPGA 385

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 06:12:35 ; Search time 464 Seconds
(without alignments)
361.683 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGARPPPLLEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pdb.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pdb.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pdb.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pdb.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pdb.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pdb.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pdb.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pdb.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pdb.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pdb.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pdb.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pdb.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pdb.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pdb.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pdb.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pdb.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11 NEW PUB.pdb.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60 NEW PUB.pdb.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	96.1	591	14	US-10-267-730-20
2	2187	95.8	591	9	US-09-943-446-7
3	2146	94.0	591	9	US-09-943-446-8
4	2008	88.0	593	9	US-09-943-446-9
5	2008	88.0	593	14	US-10-225-567A-229
6	2008	88.0	593	16	US-10-723-860-1006
7	2008	88.0	593	17	US-10-505-486-13
8	2002	87.7	593	10	US-09-826-509-563
9	2002	87.7	593	14	US-10-267-730-21
10	2002	87.7	593	17	US-10-925-095-563
11	1957	85.7	595	9	US-09-943-446-6

12	1710	74.9	585	14	US-10-267-730-19	Sequence 19, Appl
13	1698	74.4	964	14	US-10-017-161-710	Sequence 710, App
14	1698	74.4	964	15	US-10-292-798-622	Sequence 622, App
15	1551	67.9	515	14	US-10-267-730-18	Sequence 18, Appl
16	1465	64.2	536	14	US-10-372-095-2	Sequence 2, Appli
17	1130	49.5	542	14	US-10-372-095-4	Sequence 4, Appli
18	1068	46.8	575	14	US-10-372-095-5	Sequence 5, Appli
19	1050.5	46.0	550	14	US-10-225-567A-227	Sequence 227, App
20	1050.5	46.0	550	15	US-10-295-027-526	Sequence 526, App
21	1050.5	46.0	550	15	US-10-295-027-851	Sequence 851, App
22	1050.5	46.0	550	16	US-10-723-860-2139	Sequence 2139, Ap
23	1050.5	46.0	561	15	US-10-295-027-524	Sequence 524, App
24	1044.5	45.8	550	10	US-09-826-509-565	Sequence 565, App
25	1044.5	45.8	550	17	US-10-925-095-565	Sequence 565, App
26	1036	45.4	541	9	US-09-996-569-2	Sequence 2, Appli
27	1036	45.4	541	17	US-10-921-218-2	Sequence 21, Appli
28	1028.5	45.1	550	14	US-10-014-162-110	Sequence 110, App
29	1011.5	44.3	546	14	US-10-014-162-109	Sequence 109, App
30	776	34.0	459	16	US-10-831-393-4	Sequence 4, Appli
31	775.5	34.0	1324	9	US-09-935-371-56	Sequence 56, Appli
32	773.5	33.9	444	16	US-10-831-393-6	Sequence 6, Appli
33	772	33.8	459	16	US-10-831-393-3	Sequence 3, Appli
34	772	33.8	459	16	US-10-831-393-8	Sequence 8, Appli
35	762.5	33.4	458	16	US-10-831-393-5	Sequence 5, Appli
36	762.5	33.4	458	16	US-10-831-393-7	Sequence 7, Appli
37	757.5	33.2	449	15	US-10-051-874-68	Sequence 68, Appl
38	752.5	33.0	457	14	US-10-225-567A-469	Sequence 469, App
39	752.5	33.0	457	15	US-10-292-798-618	Sequence 618, App
40	752.5	33.0	457	16	US-10-831-393-1	Sequence 1, Appli
41	747	32.7	440	15	US-10-292-798-608	Sequence 608, App
42	747	32.7	440	15	US-10-051-874-64	Sequence 64, Appl
43	747	32.7	440	15	US-10-051-874-65	Sequence 65, Appl
44	747	32.7	440	15	US-10-398-454-3	Sequence 3, Appli
45	747	32.7	440	15	US-10-398-454-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-267-730-20
; Sequence 20, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schibani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-267-730-20

Query Match 96.1%; Score 2195; DB 14; Length 591;
Best Local Similarity 73.6%; Pred. No. 1.5e-189;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;
Qy 1 MGAARIAPSLALLCCPVLSAYAL-----25
Db 1 MGAARIAPSLALLCCPVLSAYALVDADDVFTKESQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 -----25

```
Db 61 NIMESDKGWTGTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEDNDIVCWPL 120
Qy 26 ----- 25
Db 121 GAPGEVAVPCPDYIYDFNKHGHAYRRCDRNGSMEVVPGHNRTWANYSECLKFWMTNETRE 180
Qy 26 -EVFDRGLMIYTVGYSGMSLASLTVAVLILAYFRRLHCTRNYIHHMFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSGMSLASLTVAVLILAYFRRLHCTRNYIHHMFSLFMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEAERLTEREELHIIIAQVPPPPAAAAAGYAGCRVAVTFFLYFLATNYWIL 144
Db 241 DAVLYSGFTLDEAERLTEREELHIIIAQVPPPPAAAAAGYAGCRVAVTFFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVWGVVRATLANTGCWDLSSGHKK 204
Db 241 DAVLYSGFTLDEAERLTEREELHIIIAQVPPPPAAAAAGYAGCRVAVTFFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVWGVVRATLANTGCWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVWGVVRATLANTGCWDLSSGHKK 360
Qy 205 WIIOVPILASVVLNFIINIRVLATKURETNAGRCDTROQYRKLRSTLVLVPLFGVH 264
Db 361 WIIOVPILASVVLNFIINIRVLATKURETNAGRCDTROQYRKLRSTLVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWSRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWSRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQOLPGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQOLPGHAKPG 540
Qy 385 APATETETLPTVMVAPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPTVMVAPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591

RESULT 2
US-09-943-446-7
; Sequence 7, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus No. US20020146777Alvegicus
US-09-943-446-7

Query Match 95.8%; Score 2187; DB 9; Length 591;
Best Local Similarity 73.4%; Pred. No. 8e-189;
Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSSAYALVDADDVFTKEQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEDNDIVCWPL 120
Qy 26 ----- 25
```

```
Db 121 GAPGEVAVPCPDYIYDFNKHGHAYRRCDRNGSMEVVPGHNRTWANYSECLKFWMTNETRE 180
Qy 26 -EVFDRGLMIYTVGYSGMSLASLTVAVLILAYFRRLHCTRNYIHHMFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSGMSLASLTVAVLILAYFRRLHCTRNYIHHMFSLFMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEAERLTEREELHIIIAQVPPPPAAAAAGYAGCRVAVTFFLYFLATNYWIL 144
Db 241 DAVLYSGFTLDEAERLTEREELHIIIAQVPPPPAAAAAGYAGCRVAVTFFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVWGVVRATLANTGCWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVWGVVRATLANTGCWDLSSGHKK 360
Qy 205 WIIOVPILASVVLNFIINIRVLATKURETNAGRCDTROQYRKLRSTLVLVPLFGVH 264
Db 361 WIIOVPILASVVLNFIINIRVLATKURETNAGRCDTROQYRKLRSTLVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWSRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWSRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQOLPGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQOLPGHAKPG 540
Qy 385 APATETETLPTVMVAPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPTVMVAPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591

RESULT 3
US-09-943-446-8
; Sequence 8, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-943-446-8

Query Match 94.0%; Score 2146; DB 9; Length 591;
Best Local Similarity 72.1%; Pred. No. 4.1e-185;
Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSSAYALVDADDVFTKEQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKAPGKFYPESKENKDVPTGSRRRGRPCLPEDNDIVCWPL 120
Qy 26 ----- 25
Db 121 GAPGEVAVPCPDYIYDFNKHGHAYRRCDRNGSMEVVPGHNRTWANYSECLKFWMTNETRE 180
Qy 26 -EVFDRGLMIYTVGYSGMSLASLTVAVLILAYFRRLHCTRNYIHHMFSLFMLRAASIFVK 84
```

Db 181 REVFDRLGMIYTVGYSSLSLTVAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 240
Qy 85 DAVLYSGFTLDEARLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLFLATNYWIL 144
Db 241 DAVLYSGFTLDEARLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHKK 360
Qy 205 WIIQVPIASVNLNFIINIRVLATKLRNAGCDTRQQYRKLRSLTLVLPFGVH 264
Db 361 WIIQVPIASVNLNFIINIRVLATKLRNAGCDTRQQYRKLRSLTLVLPFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540
Qy 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 435
Db 541 APAIENETIPTVTMPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 591

RESULT 4

US-09-943-446-9

; Sequence 9, Application US/09943446

; Patent No. US2002014677A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer Inc.

; APPLICANT: Cattleberry, Tessa A.

; APPLICANT: Lu, Bihong

; APPLICANT: Owen, Thomas A.

; APPLICANT: Smock, Steven L.

; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor

; FILE REFERENCE: PC10891AGR

; CURRENT APPLICATION NUMBER: US/09/943,446

; CURRENT FILING DATE: 2001-08-30

; PRIOR FILING DATE: 2000-08-30

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 593

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-09-943-446-9

Query Match 88.0%; Score 2008; DB 9; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLORPA 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLKYPESEDKAPTGSRYGRPCLPEDWHLWCPL 120
Qy 26 ----- 25
Db 121 GAFGEVVAVPCPDYIYDFNKHGHAYRCDRNGSWELVPGHNRWTWANYSECVKFLTNSTRE 180
Qy 26 ----- 25
Db 26 -EVFDRGLMIYTVGYSSLSLTVAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSSLSLTVAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 240
Qy 85 DAVLYSGFTLDEARLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLFLATNYWIL 144

Db 241 DAVLYSGATLDEARLTFEELRAIAQAPPPATAAAGYACRVAVTFEFLFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHKK 360
Qy 205 WIIQVPIASVNLNFIINIRVLATKLRNAGCDTRQQYRKLRSLTLVLPFGVH 264
Db 361 WIIQVPIASVNLNFIINIRVLATKLRNAGCDTRQQYRKLRSLTLVLPFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKP 383
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKP 540
Qy 384 GAPTETETLPTVMAVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 435
Db 541 GTPALETLETTPPAMAAPKDDGFLNGSCSGLDEASGSARPPPALLOEGWETVM 593

RESULT 5

US-10-225-567A-229

; Sequence 229, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 229

; LENGTH: 593

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-229

Query Match 88.0%; Score 2008; DB 14; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLORPA 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLKYPESEDKAPTGSRYGRPCLPEDWHLWCPL 120
Qy 26 ----- 25
Db 121 GAFGEVVAVPCPDYIYDFNKHGHAYRCDRNGSWELVPGHNRWTWANYSECVKFLTNSTRE 180
Qy 26 -EVFDRGLMIYTVGYSSLSLTVAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSSLSLTVAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 240
Qy 85 DAVLYSGFTLDEARLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTFEELRAIAQAPPPATAAAGYACRVAVTFEFLFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHKK 204

Db 301 VEGLYLSLIFMAFFSEKKYLGFTVFGWGLPAVFVAVVSVRATLANTCWDLSGSKK 360
Qy 205 WIIQVPIASVNLFILFINIIRVLATKLRNAGCDTRQQYRKLRLSTLVLPLFGVH 264
Db 361 WIIQVPIASVNLFILFINIIRVLATKLRNAGCDTRQQYRKLRLSTLVLPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKKSWSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKKSWSRWTLA 480
Qy 325 LDFKARKSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSOLPGHAKP 383
Db 481 LDFKARKSGSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLLPTATTNGHPOLPGHAKP 540
Qy 384 GAPATET-ETLPTVMAVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 435
Db 541 GTPALETLETTTPPAMAAPKDDGFLNGSCSGLDEASGPERPPALLOEWETVM 593
RESULT 6
US-10-723-860-1006
; Sequence 1006, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1006
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1006

Query Match 88.0%; Score 2008; DB 16; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWTASSTGKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
Qy 26 ----- 25
Db 121 GAGEVVAVPCPDYIYDFNHKHAYRRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
Qy 26 -EVFDRLGMIYTVGYSMASLTAVLILAYFRRLHCTRNIIHMHFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASTVAVLILAYFRRLHCTRNIIHMHFLSFMLRAVSIFVK 240
Qy 85 DAVLYSGFTLDEARLITEELHIIAQVPPPPAAAAGYACRVAVTPFFLYFLATNYYWIL 144
Db 241 DAVLYSGATLDEARLITEELRAIAQAQPPPPATAAGYACRVAVTPFFLYFLATNYYWIL 300
Qy 145 VEGLYLSLIFMAFFSEKKYLGFTIFGWGLPAVFVAVVGVVRATLANTCWDLSGSKK 204
Db 301 VEGLYLSLIFMAFFSEKKYLGFTVFGWGLPAVFVAVVSVRATLANTCWDLSGSKK 360
Qy 205 WIIQVPIASVNLFILFINIIRVLATKLRNAGCDTRQQYRKLRLSTLVLPLFGVH 264
Db 361 WIIQVPIASVNLFILFINIIRVLATKLRNAGCDTRQQYRKLRLSTLVLPLFGVH 420

Qy 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKKSWSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKKSWSRWTLA 480
Qy 325 LDFKARKSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSOLPGHAKP 383
Db 481 LDFKARKSGSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLLPTATTNGHPOLPGHAKP 540
Qy 384 GAPATET-ETLPTVMAVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 435
Db 541 GTPALETLETTTPPAMAAPKDDGFLNGSCSGLDEASGPERPPALLOEWETVM 593
RESULT 7
US-10-505-486-13
; Sequence 13, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 13
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-13

Query Match 88.0%; Score 2008; DB 17; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWTASSTGKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
Qy 26 ----- 25
Db 121 GAGEVVAVPCPDYIYDFNHKHAYRRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
Qy 26 -EVFDRLGMIYTVGYSMASLTAVLILAYFRRLHCTRNIIHMHFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASTVAVLILAYFRRLHCTRNIIHMHFLSFMLRAVSIFVK 240
Qy 85 DAVLYSGFTLDEARLITEELHIIAQVPPPPAAAAGYACRVAVTPFFLYFLATNYYWIL 144
Db 241 DAVLYSGATLDEARLITEELRAIAQAQPPPPATAAGYACRVAVTPFFLYFLATNYYWIL 300
Qy 145 VEGLYLSLIFMAFFSEKKYLGFTIFGWGLPAVFVAVVGVVRATLANTCWDLSGSKK 204
Db 301 VEGLYLSLIFMAFFSEKKYLGFTVFGWGLPAVFVAVVSVRATLANTCWDLSGSKK 360
Qy 205 WIIQVPIASVNLFILFINIIRVLATKLRNAGCDTRQQYRKLRLSTLVLPLFGVH 264
Db 361 WIIQVPIASVNLFILFINIIRVLATKLRNAGCDTRQQYRKLRLSTLVLPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKKSWSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKKSWSRWTLA 480

Qy 325 LDFKRRKSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPQHAKP 383
Db 481 LDFKRRKSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPTATTNGHPQLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435
Db 541 GTPALETLETPPMAAPKDDGFLNGSCGLDEASGSRPPPALLOEGWETVM 593

RESULT 8

US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 87.7%; Score 2002; DB 10; Length 593;
Best Local Similarity 67.1%; Pred. No. 4.4e-172;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWSASTSGKPRKDKASGLYPSEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
Qy 26 ----- 25
Db 121 GAGEVVAVPCPDYIDFNHKGHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNRE 180
Qy 26 -EVPDRGLMITYTGYSMSLASLTAVLILAYFRRLHCTRYNIHMHFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTGYSVSLASLTAVLILAYFRRLHCTRYNIHMHFLSLFMLRAVSI 240
Qy 85 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGYACRVAVTPFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEAERLTEBELRAIAQAPPPATAAGYACRVAVTPFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVAVGVVATLANTCWDLSGCHK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVAVGVVATLANTCWDLSGCHK 360
Qy 205 WIQVPIASVNLNFIINIRVLATKLRETNAGRCDTQQYRKLLRSLTLVLPFGVH 264
Db 361 WIQVPIASVNLNFIINIRVLATKLRETNAGRCDTQQYRKLLKSLPLVLPFGVH 420
Qy 265 YTFVMAIPYTEVSGTLWQIQHYEMLFNSFGGFVAIIYFCNGEVOAEIKKSWRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQVQHYEMLFNSFGGFVAIIYFCNGEVOAEIKKSWRWTLA 480
Qy 325 LDFKRRKSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPQHAKP 383
Db 481 LDFKRRKSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPTATTNGHPQLPGHAKP 540

Qy 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435
Db 541 GTPALETLETPPMAAPKDDGFLNGSCGLDEASGSRPPPALLOEGWETVM 593

RESULT 9

US-10-267-730-21
; Sequence 21, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match 87.7%; Score 2002; DB 14; Length 593;
Best Local Similarity 67.1%; Pred. No. 4.4e-172;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWSASTSGKPRKDKASGLYPSEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
Qy 26 ----- 25
Db 121 GAGEVVAVPCPDYIDFNHKGHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNRE 180
Qy 26 -EVPDRGLMITYTGYSMSLASLTAVLILAYFRRLHCTRYNIHMHFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTGYSVSLASLTAVLILAYFRRLHCTRYNIHMHFLSLFMLRAVSI 240
Qy 85 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGYACRVAVTPFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEAERLTEBELRAIAQAPPPATAAGYACRVAVTPFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVAVGVVATLANTCWDLSGCHK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVAVGVVATLANTCWDLSGCHK 360
Qy 205 WIQVPIASVNLNFIINIRVLATKLRETNAGRCDTQQYRKLLRSLTLVLPFGVH 264
Db 361 WIQVPIASVNLNFIINIRVLATKLRETNAGRCDTQQYRKLLKSLTLVLPFGVH 420
Qy 265 YTFVMAIPYTEVSGTLWQIQHYEMLFNSFGGFVAIIYFCNGEVOAEIKKSWRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQVQHYEMLFNSFGGFVAIIYFCNGEVOAEIKKSWRWTLA 480
Qy 325 LDFKRRKSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPQHAKP 383
Db 481 LDFKRRKSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPTATTNGHPQLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435

Db 541 GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGPERPPALLQBEWETVM 593

RESULT 10

US-10-925-095-563
; Sequence 563, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-563

Query Match 87.7%; Score 2002; DB 17; Length 593;
Best Local Similarity 67.1%; Pred. No. 4.4e-172;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWTASSTGKPKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHLWCWPL 120
Qy 26 ----- 25
Db 121 GAPEVVAVPCPDYIYDFNHKGHAYRCDRNGSWELVPGHNRITWANYSECVKFLTNETRE 180
Qy 26 -EVFDRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNYYIHMHPLSFMRLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASTVAVLILAYFRRLHCTRNYYIHMHPLSFMRLRAVSIFVK 240
Qy 85 DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAGYACRVAVTFEFLYFLATNYYWIL 144
Db 241 DAVLYSGATLDEAERLTERELRAIAQAAPPPTAAAGYACRVAVTFEFLYFLATNYYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLGPVAVFVAVVGVVRATLANTCWDLSGSHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLGPVAVFVAVVSVRATLANTCWDLSGSHKK 360
Qy 205 WIIQVPILASVILNFILFINIRVATKLRNAGRCDTTQQYRKLRLSTLVLPLPGVH 264
Db 361 WIIQVPILASVILNFILFINIRVATKLRNAGRCDTTQQYRKLRLKSLVLMLPLPGVH 420
Qy 265 YTVFMAIPYTVESGTLNQIQMHYEMLENSFGQFPVAILIYFCNGEVOAEIRKKSWSRWTLA 324
Db 421 YIVFMATPYTVESGTLNQIQMHYEMLENSFGQFPVAILIYFCNGEVOAEIRKKSWSRWTLA 480
Qy 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATTNGHSOLPGHAKP 383
Db 481 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPLTATTNGHPQLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAYPKDDGFLNGSCSGLDEASGSRPPPLLOEWETVM 435
Db 541 GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGPERPPALLQBEWETVM 593

RESULT 11

US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Query Match 85.7%; Score 1957; DB 9; Length 595;
Best Local Similarity 65.8%; Pred. No. 5.2e-168;
Matches 394; Conservative 11; Mismatches 24; Indels 172; Gaps 5;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 DIMESDKGWASASTSGKPKKASGLYPESEEDKEVPTGSRHRGRPCLPEDWHLWCWPL 120
Qy 26 ----- 25
Db 121 GAPEVVAVPCPDYIYDFNHKGHAYRCDRNGSWELVPGHNRITWANYSECVKFLTNETRE 180
Qy 26 -EVFDRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNYYIHMHPLSFMRLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASTVAVLILAYFRRLHCTRNYYIHMHPLSFMRLRAVSIFVK 240
Qy 85 DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAGYACRVAVTFEFLYFLATNYYWIL 144
Db 241 DAVLYSGATLDEAERLTERELRAIAQAAPPPTAAAGYACRVAVTFEFLYFLATNYYWIL 299
Qy 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLGPVAVFVAVVGVVRATLANTCWDLSGSHKK 204
Db 300 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLGPVAVFVAVVSVRATLANTCWDLSGSHKK 359
Qy 205 WIIQVPILASVILNFILFINIRVATKLRNAGRCDTTQQYRKLRLSTLVLPLPGVH 264
Db 360 WIIQVPILASVILNFILFINIRVATKLRNAGRCDTTQQYRKLRLKSLVLMLPLPGVH 419
Qy 265 YTVFMAIPYTVESGTLNQIQMHYEMLENSFGQFPVAILIYFCNGEVOAEIRKKSWSRWTLA 324
Db 420 YIVFMATPYTVESGTLNQIQMHYEMLENSFGQFPVAILIYFCNGEVOAEIRKKSWSRWTLA 479
Qy 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLPP-----ATTNGHSOL 377
Db 480 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLPLSPRLPLPAAAAATTATTNGHPP 539
Qy 378 PGHAKPGAPATETETLPVT---NAVPKDDGFLNGSCSGLDEASGSRPPPLLOEWETV 434
Db 540 PGHTKGPAP-----TLPATPPATAAPKDDGFLNGSCSGLDEASAPERPALLQBEWETV 594
Qy 435 M 435
Db 595 M 595


```

; PRIOR APPLICATION NUMBER: JP 2001/246789
;
; PRIOR FILING DATE: 2001-06-18
;
; NUMBER OF SEQ ID NOS: 2430
;
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 710
;
; LENGTH: 964
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; US-10-017-161-710

```

Query Match	74.4%;	Score 1698;	DB 14;	Length 964;
Best Local Similarity	59.9%;	Pred. No. 2.6e-144;		
Matches 356;	Conservative 11;	Mismatches 31;	Indels 196;	Gaps 9
QY	26	EVFDRLGMIYTGYSMSLASLTAVAILAYF-----	56	
DB	317	EVFDRLGMIYTGYSVSLASLTAVAILAYFRWAGRCRRRRDMVEGGRWPRSDATPSLHP	376	
QY	57	-----RRLHCTRNTHHMFSLFMLRAASIF	82	
DB	377	SPDAGVPTYGAQPSFLSTRASPCHPHRSCRAPRRRLHCTRNTHHMLFLSFLMLRAVSIF	436	
QY	83	VKDAILYSGFTLEAERLLEEELHIIAQVPPPPAAAAAGVAG-----	124	
DB	437	VKDAILYSGATLEAERLLEEELURAAQAPPPATAAGVSTPLPARSCRHWPRGAPP	496	
QY	125	-----CR-----	126	
DB	497	RPAPRSPCPPPASATGFSHNSNPSYVRPNPQLCRRPCCOGLRVSHTPRAAIKAPTSTQ	556	
QY	127	VATFFLYFLATNYWILVEGLYLHSLIFMAFPSEKKYLGFTIFGWLPAVFVAVWGV	186	
DB	557	VATFFLYFLATNYWILVEGLYLHSLIFMAFPSEKKYLGFTVFGWGLPAVFVAVWVS	616	
QY	187	RATLANTGCWDLSSGHKKWIIQVPIIASVU--LNFILFINIIRVLATKLRETNAGRC	244	
DB	617	RATLANTG-----VQPDRAAPSLPQNFILFINIVRLATKLRETNAGRC	664	
QY	245	QOY-----RKLLRSTLVLPLFGVHYTVFMALPTEVSGTLWQIQMHYEML	290	
DB	665	QOYRGSGIALTYLPRWPKLLKSTLVLMLFGVHYIVFMATPTEVSGTLWQVQMHYEML	724	
QY	291	FNSF-----QQFFVAILIYFCNGEVOAIBIRKSWSHWTL	323	
DB	725	FNSFQVRSAGPGIAEGGRSGGRPSDRHPSSQGFVAILIYFCNGEVOAIEIKESWSRWTL	784	
QY	324	ALDPKPKAKSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTTNGHSLPGHAK	382	
DB	785	ALDPKPKAKSGSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLLPATTTNGHQLPGHAK	844	
QY	383	PGAPATET-ETLPVTWAVPKDGFNGSCGLDEERASGSRPPLPQEGHWETVM	435	
DB	845	PGTPALETLETTTPPAAAPKDKGFLNGSCGLDEERASGSRPPLPQEGHWETVI	898	

```

RESULT 14
US-10-292-798-622
; Sequence 622, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIKYO
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ASURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 08435/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070

```

```

RESULT 12
US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match          74.9%; Score 1710; DB 14; Length 585;
Best Local Similarity 80.2%; Pred. No. 1.1e-145;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;

Qy      26  EVFDRLGMIYTVGVSGMSLASLTVAVLILAYPRRLHCTRNYYIHMMFLSFMLRAASIFPKD 85
Db      179 EVFDRLGMIYTVGVSGISLGSLTVAVLILGYPRRLHCTRNYYIHMHFLFVSFMLRAVSIPIKD 238

Qy      86  AVLYSGFTLDEAERLTSEELHIIAQVPPPPAAAAAGVAGCRAVATFFLYFLATNYYILV 145
Db      239 AVLYSGYSTDEIERITBEELRAFTF--PPADKA-GFVGCRAVATVFLYFLTNNYYILV 295

Qy      146  EGLYLHSLIPMAFPSEKKYLWGPTIPQGLPAVFVAWVGVRATYANTGCWDLSSGHKKW 205
Db      296  EGLYLHSLIPMAFPSEKKYLWGPTLFGWGLPAVFVAWVTVRATLANTECWDLSSGNKKW 355

Qy      206  IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCDTQQRKLLRSTLVLPFLGVHY 265
Db      356  IIQVPILAAIVWNFIILFINIIRVLATKLRETNAGRCDTQQRKLLKSTLVLPFLGVHY 415

Qy      266  TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILYFCNGEVOAEIRKWSRWTLL 325
Db      416  IVFMATPYTEVSGTLWQVQMHYEMLFNSFGQFFVAILYFCNGEVOAEIKKWSRWTLL 475

Qy      326  DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSIPLSPRLPP--ATTNGHSOLPGHAK 382
Db      476  DFKRKARSGSSSYSGPMVSHTSVTNVGPRGLALSISPLAPAGAGASANGHQDPGVK 535

Qy      383  PGAPATETETLPVTMAVP--KDDGFLNGSCSGLDEEASGSARPPLPLQEGWETYM 435
Db      536  HG--SISGNSLPSSGPGPGTKDDCYLNG--SGLYEPMVGE--OPPLLEEREETVM 585

```

RESULT 13
US-10-017-161-710
; Sequence 710, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 094335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-798-622

Query Match      74.4%; Score 1698; DB 15; Length 964;
Best Local Similarity 59.9%; Pred. No. 2.6e-144;
Matches 356; Conservative 11; Mismatches 31; Indels 196; Gaps 9;

Qy 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYF----- 56
Db 317 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRWAGRRERRDMVEGGRWPRSDATPSLHP 376
Qy 57 -----RRLHCTRNTHMMFLSFMRLRAASIF 82
Db 377 SPPAGVPTYGAQPSFLSTRASPCPHPRSCRAPRRRLHCTRNTHMHLFLSFMRLRAVSIF 436
Qy 83 VKDAVLYSGFTLDEAERLITEELHIIAQVPPPPAAAAGVAG----- 124
Db 437 VKDAVLYSGATLDEAERLITEELRAIAQAPPPATAAAGTVSTPLPARSCRHWPRGAPP 496
Qy 125 -----CR----- 126
Db 497 RPAPARSPCPPASATGFSHNSPYRVRPNPQLCRPCCQGLRVSHSTPRAAIKAPTSTQ 556
Qy 127 VAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGV 186
Db 557 VAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVSV 616
Qy 187 RATLANTGCWDLSSGHKKWIIQVPILASVV--LNFILFINIIRVLATKLRETNAGRCDDR 244
Db 617 RATLANTG-----VQPPDAAPSLPQLNFILFINIIRVLATKLRETNAGRCDDR 664
Qy 245 QQY-----RKLRLSTLVLPVLFVGHVTVFMALPYTEVSGTLWQIQMHYEML 290
Db 665 QQYRGSGSLATYLPWRPKLLKSLVLMPLFGVHYIVFMATPYTEVSGTLWQVQMHYEML 724
Qy 291 FNSF-----QQFFVAILIYFCNGEVOAEIRKSWSRWTL 323
Db 725 FNSFQVRSAGPLAEGRGSGRSDSRHPSQGGFFVAILIYFCNGEVOAEIRKSWSRWTL 784
Qy 324 ALDFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLPLSPR-LPPATTNGHSQLPQGHAK 382
Db 785 ALDFKRRKARSGSSSYSGPMVSHSTVTVNGPRVGLGLPLSPRLPLPTATTNGHPQLPGHAK 844
Qy 383 PGAPATET-ETLPVTMAVPPKDDGLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
Db 845 PGTPALETLETPPMAAPKDDGFLNGSCSGLDEEASGSPRPALLQEEWETVI 898

RESULT 15
US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
```

```
; TYPE: PRT
; ORGANISM: Didelphoidea
; US-10-267-730-18

Query Match      67.9%; Score 1551; DB 14; Length 515;
Best Local Similarity 86.6%; Pred. No. 2.3e-131;
Matches 291; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

Qy 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRELHCTRNTHMHLFVSMRLRAASIFVKD 85
Db 179 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRELHCTRNTHMHLFVSMRLRAVSIFIKD 238
Qy 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 145
Db 239 AVLYSGVSTDEIRITEELRAFTE--PPADKA-GFVGCRAVTVFLYFLTNTNYWILV 295
Qy 146 EGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVRAVTLANTGCWDLSSGHKKW 205
Db 296 EGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVTVRATLANTECWDLSGNGKKW 355
Qy 206 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDDRQOYRKLRLSTLVLPFGVHY 265
Db 356 IIQVPILAIVNFINIIRVLATKLRETNAGRCDDRQOYRKLRLSTLVLPFGVHY 415
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGGFFVAILIYFCNGEVOAEIRKSWSRWTL 325
Db 416 IVFMATPYTEVSGTLWQVQMHYEMLFNSFGGFFVAILIYFCNGEVOAEIRKSWSRWTL 475
Qy 326 DFRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLP 361
Db 476 DFRRKARSGSSSYSGPMVSHSTVTVNGPRGWPCCP 511
```

Search completed: July 4, 2005, 06:27:00
Job time : 467 secs

QY 145 VEGYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVVGVVGRATLANTCGWDLSSGHKK 204
DB 301 VEGYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVVGVVGRATLANTCGWDLSSGHKK 360
QY 205 WIIQVPIASVVLNFIILFIIIRVLATKLRNAGRCDTQQRKLLRSLTLVLPFGVH 264
DB 361 WIIQVPIASVVLNFIILFIIIRVLATKLRNAGRCDTQQRKLLRSLTLVLPFGVH 420
QY 265 YTVFMALPYTEVSGTLQWIOHMYEMLFNSQGFVFAIYFCFCNGEVOAEIRKSWRWTLA 324
DB 421 YTVFMALPYTEVSGTLQWIOHMYEMLFNSQGFVFAIYFCFCNGEVOAEIRKSWRWTLA 480
QY 325 LDFKFKARSGSSSYSGPMVSHSTVTVNGVRAGISLPLSPRLPPATNNGHSQLPGHAKPG 384
DB 481 LDFKFKARSGSSSYSGPMVSHSTVTVNGVRAGISLPLSPRLPPATNNGHSQLPGHAKPG 540
QY 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
DB 541 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591
RESULT 2
S44203
parathyroid hormone-related peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S44203
R;Karpierien, M.; van Dijk, T.B.; Hoelmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boonstra
submitted to the EMBL Data Library, April 1994
A;Description: Expression pattern of parathyroid hormone/parathyroid hormone related pep
A;Reference number: S44203
A;Accession: S44203
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-591 <AR>
A;Cross-references: UNIPROT:P41593; EMBL:X78936; NID:G474828; PIDN:CAA55536.1; PID:G4748
C;Superfamily: glucagon receptor
Query Match 94.0%; Score 2146; DB 2; Length 591;
Best Local Similarity 72.1%; Pred. No. 8.9e-171;
Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSAVAL----- 25
DB 1 MGTARIAPSLALLCCPVLSAVALVDADVTFKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
DB 61 NIMESDKGWTGTPASTSGKPRKEAPGKFPYPSKENKDVPTGSRRRGRPCLPEDWNIWCWPL 120
QY 26 ----- 25
DB 121 GAGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPVGHNRWTANYSECLKFMTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNIIHMHFLSFMRLAASIFVK 84
DB 181 REVFDRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNIIHMHFLSFMRLAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVACRVAVTFFLYFLATNYYWIL 144
DB 241 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVACRVAVTFFLYFLATNYYWIL 300
QY 145 VEGYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVVGVVGRATLANTCGWDLSSGHKK 204
DB 301 VEGYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVVGVVGRATLANTCGWDLSSGHKK 360
QY 205 WIIQVPIASVVLNFIILFIIIRVLATKLRNAGRCDTQQRKLLRSLTLVLPFGVH 264
DB 361 WIIQVPIASVVLNFIILFIIIRVLATKLRNAGRCDTQQRKLLRSLTLVLPFGVH 420
QY 265 YTVFMALPYTEVSGTLQWIOHMYEMLFNSQGFVFAIYFCFCNGEVOAEIRKSWRWTLA 324
DB 421 YTVFMALPYTEVSGTLQWIOHMYEMLFNSQGFVFAIYFCFCNGEVOAEIRKSWRWTLA 480
QY 325 LDFKFKARSGSSSYSGPMVSHSTVTVNGVRAGISLPLSPRLPPATNNGHSQLPGHAKPG 384
DB 481 LDFKFKARSGSSSYSGPMVSHSTVTVNGVRAGISLPLSPRLPPATNNGHSQLPGHAKPG 540
QY 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
DB 541 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591

DB 421 YTVFMALPYTEVSGTLQWIOHMYEMLFNSQGFVFAIYFCFCNGEVOAEIRKSWRWTLA 480
QY 325 LDFKFKARSGSSSYSGPMVSHSTVTVNGVRAGISLPLSPRLPPATNNGHSQLPGHAKPG 384
DB 481 LDFKFKARSGSSSYSGPMVSHSTVTVNGVRAGISLPLSPRLPPATNNGHSQLPGHAKPG 540
QY 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
DB 541 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591
RESULT 3
I59297
parathyroid hormone/parathyroid hormone related-peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59297
R;McCuaiig, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A;Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyroid
A;Reference number: I59297; MUID:94255468; PMID:8197183
A;Accession: I59297
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-589 <RES>
A;Cross-references: UNIPROT:P41593; GB:L34611; NID:G530149; PIDN:AAA40011.1; PID:G530151
C;Genetics:
A;Gene: PTHR
A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 451
C;Superfamily: glucagon receptor
Query Match 93.5%; Score 2134; DB 2; Length 589;
Best Local Similarity 72.1%; Pred. No. 8.9e-170;
Matches 426; Conservative 1; Mismatches 6; Indels 158; Gaps 2;
QY 1 MGAARIAPSLALLCCPVLSAVAL----- 25
DB 1 MGTARIAPSLALLCCPVLSAVALVTSDVTFKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
DB 61 NIMESDKGWTGTPASTSGKPRKEAPGKFPYPSKENKDVPTGSRRRGRPCLPEDWNIWCWPL 120
QY 26 ----- 25
DB 121 GAGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPVGHNRWTANYSECLKFMTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNIIHMHFLSFMRLAASIFVK 84
DB 181 REVFDRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNIIHMHFLSFMRLAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVACRVAVTFFLYFLATNYYWIL 144
DB 241 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVACRVAVTFFLYFLATNYYWIL 300
QY 145 VEGYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVVGVVGRATLANTCGWDLSSGHKK 204
DB 301 VEGYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVVGVVGRATLANTCGWDLSSGHKK 360
QY 205 WIIQVPIASVVLNFIILFIIIRVLATKLRNAGRCDTQQRKLLRSLTLVLPFGVH 264
DB 361 WIIQVPIASVVLNFIILFIIIRVLATKLRNAGRCDTQQRKLLRSLTLVLPFGVH 420
QY 265 YTVFMALPYTEVSGTLQWIOHMYEMLFNSQGFVFAIYFCFCNGEVOAEIRKSWRWTLA 324
DB 421 YTVFMALPYTEVSGTLQWIOHMYEMLFNSQGFVFAIYFCFCNGEVOAEIRKSWRWTLA 478
QY 325 LDFKFKARSGSSSYSGPMVSHSTVTVNGVRAGISLPLSPRLPPATNNGHSQLPGHAKPG 384
DB 479 LDFKFKARSGSSSYSGPMVSHSTVTVNGVRAGISLPLSPRLPPATNNGHSQLPGHAKPG 538
QY 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
DB 541 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591

Db 539 APAIENETIPVTWTPKDDGFLNGSCGLDEASGSARPPPLQEWETVM 589

RESULT 4
A49191
parathyroid hormone/PTH-related peptide receptor - human
N;Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: I38139; A49191; I38113; G01562; S29610
R;Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuurmann, M.
Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995
A;Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons
A;Reference number: I38139; MUID:95263723; PMID:7745008
A;Accession: I38139
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-593 <RES>
A;Cross-references: UNIPROT:Q03431; EMBL:U22409; NID:9897594; PIDN:AAB60657.1; PID:9897594
R;Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.
Endocrinology 132, 2157-2165, 1993
A;Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa
A;Reference number: A49191; MUID:93238641; PMID:8386612
A;Accession: A49191
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-593 <CH>
A;Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722
A;Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIPI:130234)
R;Schneider, H.; Feyen, J.H.; Seuwen, K.; Movva, N.R.
Eur. J. Pharmacol. 246, 149-155, 1993
A;Title: Cloning and functional expression of a human parathyroid hormone receptor.
A;Reference number: I38113; MUID:93387403; PMID:8397094
A;Accession: I38113
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-593 <RES>
A;Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813
R;Levine, M.
submitted to the EMBL Data Library, November 1994
A;Reference number: G07787
A;Accession: G01562
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-593 <LEV>
A;Cross-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130
C;Genetics:
A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 88.0%; Score 2008; DB 2; Length 593;
Best Local Similarity 67.3%; Pred. No. 2.8e-159;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSAYALVDADVMTKEEQIFLLHRAQAQCEKKLKEVLORPA 60
Qy 26 ----- 25
Db 61 SIMESDKWTSASTSGKPRKDKASGLKYPESEEDKEAPTGSRYGRPCLPEDHILCWPL 120
Qy 26 ----- 25
Db 121 GAGGEVAVPCPDVIYDFPNHGHAYRCDNRGWSWELVPGHNRWTWANYSECVKFLTNRE 180
Qy 26 -EVDRLGMIYTCVGSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVK 84
Db 181 REVDRLGMIYTCVGSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVK 240
Qy 85 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAVAGCRVAVTFFLYFLATNYWIL 144

Db 241 DAVLYSGATLDEAERLTHEELHIIAQVPPPPAAAAVAGCRVAVTFFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLWGFTTFGWGLPAVFAVAVVGVVRATLANTCWDLSGGHK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTTFGWGLPAVFAVAVVGVVRATLANTCWDLSGG 360
Qy 205 WIIQVPIASVILNFILFINIRVLATKRETNAGRCDDTQQYRKLRSLTLVLPFGVH 264
Db 361 WIIQVPIASVILNFILFINIRVLATKRETNAGRCDDTQQYRKLRSLTLVLPFGVH 420
Qy 265 YTFMALPYTEVSGTLWQIMHYEMLFNSFGQFVAILIYFCNGEVOAEIRKSWRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIMHYEMLFNSFGQFVAILIYFCNGEVOAEIRKSWRWTLA 480
Qy 325 LDFKRAKSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATYNGHSOLPGHAKP 383
Db 481 LDFKRAKSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATYNGHSOLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLQEWETVM 435
Db 541 GTPALETLETPPMAAPKDDGFLNGSCGLDEASGSARPPPLQEWETVM 593

RESULT 5
A39286
parathyroid hormone / parathyroid hormone-related peptide - North American opossum
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: A39286
R;Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K.
Science 254, 1024-1026, 1991
A;Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel
A;Reference number: A39286; MUID:92054592; PMID:1658941
A;Accession: A39286
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-585 <JUE>
A;Cross-references: UNIPROT:P25107; GB:M74445
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 74.9%; Score 1710; DB 2; Length 585;
Best Local Similarity 80.2%; Pred. No. 1.8e-134;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;

Qy 26 EVDRLGMIYTCVGSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 85
Db 179 EVDRLGMIYTCVGSMSLSGLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFIKD 238
Qy 86 AVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAVAGCRVAVTFFLYFLATNYWILV 145
Db 239 AVLYSGVSTDEIRITEELRAETE--PPADKA-GFVGCRVAVTFFLYFLATNYWILV 295
Qy 146 EGYLHSLIFMAFFSEKKYLWGFTTFGWGLPAVFAVAVVGVVRATLANTCWDLSGGHKW 205
Db 296 EGYLHSLIFMAFFSEKKYLWGFTTFGWGLPAVFAVAVVGVVRATLANTCWDLSGGKWK 355
Qy 206 IIOVPIASVILNFILFINIRVLATKRETNAGRCDDTQQYRKLRSLTLVLPFGVHY 265
Db 356 IIOVPIAAIVNFILFINIRVLATKRETNAGRCDDTQQYRKLRSLTLVLPFGVHY 415
Qy 266 TVFMALPYTEVSGTLWQIMHYEMLFNSFGQFVAILIYFCNGEVOAEIRKSWRWTLAL 325
Db 416 IVFMATPYTEVSGTLWQIMHYEMLFNSFGQFVAILIYFCNGEVOAEIRKSWRWTLAL 475
Qy 326 DFKRAKSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPP---ATTNGHSOLPGHAK 382
Db 476 DFKRAKSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPP-LPGAGASANGHQLPGYVK 535
Qy 383 PGAPATETETLPVTMAVP--KDDGFLNGSCGLDEASGSARPPPLQEWETVM 435
Db 536 HG--SISENSLPSSGPEFGTKDDGYLNG--SGLYEPMVGE--QPPFLLEERETVM 585

RESULT 6
A57519
Parathyroid hormone receptor 2 precursor - human
N:Alternate names: PTH2 receptor
C:Species: Homo sapiens (man)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C:Accession: A57519
R:Udgin, T.B.; Gruber, C.; Bonner, T.I.
J. Biol. Chem. 270, 15455-15458, 1995
A:Title: Identification and functional expression of a receptor selectively recognizing
A:Reference number: A57519; MUID:95318121; PMID:7797535
A:Accession: A57519
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-550 <USD>
A:Cross-references: UNIPROT:P49190; GB:U25128; NID:g9887966; PIDN:AAC50157.1; PID:g9887967
C:Genetics:
A:Gene: GDB:PTH22; PTHR2R
A:Cross-references: GDB:731977; OMIM:601469
A:Map position: 2q33-2q33
C:Superfamily: glucagon receptor
C:Keywords: hormone receptor

Query Match 46.0%; Score 1050.5; DB 2; Length 550;
Best Local Similarity 53.9%; Pred. No. 1.4e-79;
Matches 208; Conservative 58; Mismatches 85; Indels 35; Gaps 7;

Qy 26 EVFDRIGMIVTVGYSMSLASITVAVILAYFRLHCTRTNYIHMFSLFMRASIFVKD 85
Db 139 EFERLYVMYTVGISISFGSLAVAILIIGYFRLHCTRTNYIHMLFVSFMRATSIKVD 198
Qy 86 AVLYSGFTDABRLTEELHIIAQVPPPPAAAAGV-----YACRVAVTFEFLYFLATNY 140
Db 199 RVHAHIGVKELES-----IQDDPQNSIEATSDVSKQYIGCKIAVWFIYFLATNY 251
Qy 141 YWILVEGLYLHSLIFMAFFSEKKYLGWFTTFPGWGLPAFVAVVWVGRATLANTGCDLSS 200
Db 252 YWILVEGLYLHNLIFVAFPSDTKYLGWFTTFPGWGLPAFVAVVWVGRATLADARCWLSA 311
Qy 201 GHKWIITQVPLASVNLFINIIRVLATKLRETNAGRCDDTQOYRKLRLSTLVLVPL 260
Db 312 GDIKWITQAPILAAIGLNFILFNLTVRLATKIWETNAVGHDRKQYRKLAKSTLVLV 371
Qy 261 FGVIHYTFMALPYTEVSGTLQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320
Db 372 FGVIHYTFVCLPHS-FTGLGWEIRMHCELPFNSFGQFFVAILIYFCNGEVOAEIRKWSR 430
Qy 321 WTALDFPKRKARSGS-----SSYSYSGPMVSHTSVTNVGPRAGLSPLSPRLPP 368
Db 431 WNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQVAASTRWLI---SGKAATIASRQP- 486
Qy 369 ATTNGHSQLCHAKGAPATETILP 394
Db 487 ---DSHTITLPGYWSN---SEQDCLP 506

RESULT 7
JH0594
vasoactive intestinal peptide receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: JH0594; S56014
R:Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A:Title: Functional expression and tissue distribution of a novel receptor for vasoactive
A:Reference number: JH0594; MUID:92232309; PMID:1314625
A:Accession: JH0594
A:Molecule type: mRNA
A:Residues: 1-459 <ISH>
A:Cross-references: UNIPROT:P30083; GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641
A:Experimental source: lung

Query Match 46.0%; Score 1050.5; DB 2; Length 550;
Best Local Similarity 53.9%; Pred. No. 1.4e-79;
Matches 208; Conservative 58; Mismatches 85; Indels 35; Gaps 7;

Qy 26 EVFDRIGMIVTVGYSMSLASITVAVILAYFRLHCTRTNYIHMFSLFMRASIFVKD 85
Db 139 EFERLYVMYTVGISISFGSLAVAILIIGYFRLHCTRTNYIHMLFVSFMRATSIKVD 198
Qy 86 AVLYSGFTDABRLTEELHIIAQVPPPPAAAAGV-----YACRVAVTFEFLYFLATNY 140
Db 199 RVHAHIGVKELES-----IQDDPQNSIEATSDVSKQYIGCKIAVWFIYFLATNY 251
Qy 141 YWILVEGLYLHSLIFMAFFSEKKYLGWFTTFPGWGLPAFVAVVWVGRATLANTGCDLSS 200
Db 252 YWILVEGLYLHNLIFVAFPSDTKYLGWFTTFPGWGLPAFVAVVWVGRATLADARCWLSA 311
Qy 201 GHKWIITQVPLASVNLFINIIRVLATKLRETNAGRCDDTQOYRKLRLSTLVLVPL 260
Db 312 GDIKWITQAPILAAIGLNFILFNLTVRLATKIWETNAVGHDRKQYRKLAKSTLVLV 371
Qy 261 FGVIHYTFMALPYTEVSGTLQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320
Db 372 FGVIHYTFVCLPHS-FTGLGWEIRMHCELPFNSFGQFFVAILIYFCNGEVOAEIRKWSR 430
Qy 321 WTALDFPKRKARSGS-----SSYSYSGPMVSHTSVTNVGPRAGLSPLSPRLPP 368
Db 431 WNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQVAASTRWLI---SGKAATIASRQP- 486
Qy 369 ATTNGHSQLCHAKGAPATETILP 394
Db 487 ---DSHTITLPGYWSN---SEQDCLP 506

R;Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A:Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5'
A:Reference number: S56014; MUID:97104266; PMID:8948424
A:Accession: S56014
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-26 <PBI>
A:Cross-references: EMBL:U10635; NID:g505752; PIDN:AAB48185.1; PID:g514311
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F:146-168/Domain: transmembrane #status predicted <TM1>
F:176-195/Domain: transmembrane #status predicted <TM2>
F:218-241/Domain: transmembrane #status predicted <TM3>
F:256-277/Domain: transmembrane #status predicted <TM4>
F:295-318/Domain: transmembrane #status predicted <TM5>
F:344-363/Domain: transmembrane #status predicted <TM6>
F:376-395/Domain: transmembrane #status predicted <TM7>
F:58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.8%; Score 772; DB 2; Length 459;
Best Local Similarity 44.8%; Pred. No. 1.7e-56;
Matches 147; Conservative 64; Mismatches 83; Indels 34; Gaps 7;

Qy 35 YTVGYSMSLASITVAVILAYFRLHCTRTNYIHMFSLFMRASIFVKDVLVSGFTL 94
Db 147 YTVGYSMSLASITVAVILAYFRLHCTRTNYIHMFSLFMRASIFVKDVLVSGFTL 206
Qy 95 DEARLITEBELHIIAQVPPPPAAAAGVACRVAVTFEFLYFLATNYIWLVEGLYLHSLI 154
Db 207 DHCSEAS-----VGCKAAVVFQYCVMANFVLLVLEGLYLYTL 245
Qy 155 FMAFFSEKKYLGWFTTFPGWGLPAFVAVVWVGRATLANTGCD-LSGCHKWIIQVPILA 213
Db 246 AVSFFSEKKYLGWFTTFPGWGLPAFVAVVWVGRATLANTGCD-LSGCHKWIIQVPILA 305
Qy 214 SVVNLFINIIRVLATKLRETNAGRCDDTQOYRKLRLSTLVLVPLFGVHYTFVFMALPY 273
Db 306 SILVNFVLCIIRILVQLRPPDICKNDS-SPYSRLAKSTLILIPFGHYVWFAPFP- 363
Qy 274 TEVSGTLQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSRWTI--ALDFPKKA 331
Db 364 ---DNFKAQVQVWFELVWGSFGQFFVAILIYFCNGEVOAEIRKWSRWTI--ALDFPKKA 420
Qy 332 R---SGSSSYSGPMVSHTSVTNVGPR 356
Db 421 QHPWGGNGATCSTQVS--MLTRVSPSA 446

RESULT 8
S16319
secretin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S16319
R:Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO J. 10, 1635-1641, 1991
A:Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A:Reference number: S16319; MUID:91266890; PMID:1646711
A:Accession: S16319
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-449 <ISH>
A:Cross-references: UNIPROT:P23811; EMBL:X59132; NID:g57228; PIDN:CAAA1849.1; PID:g57229
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.2%; Score 757.5; DB 2; Length 449;
Best Local Similarity 44.8%; Pred. No. 2.7e-55;
Matches 154; Conservative 64; Mismatches 87; Indels 39; Gaps 9;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 02:53:08 ; Search time 90 Seconds
(without alignments)
2475.049 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EAGSARPPPLQGMETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2187	95.8	591	1 PRRR_RAT	P25961 rattus norv
2	2156	94.4	591	2 Q80W08	Q80W08 mus musculu
3	2148	94.1	591	2 Q91WV4	Q91WV4 mus musculu
4	2146	94.0	591	1 PRRR_MOUSE	P41593 mus musculu
5	2008	88.0	593	1 PRRR_HUMAN	Q03431 homo sapien
6	1957	85.7	595	2 Q9TUJ1	Q9TUJ1 canis famil
7	1932	84.6	589	2 Q7YR13	Q7YR13 cervus elap
8	1925	84.3	585	1 PRRR_PIG	P50133 sus scrofa
9	1710	74.9	585	1 PRRR_DIDWA	P25107 didelphis m
10	1698	74.4	964	2 Q8NH54	Q8NH54 homo sapien
11	1465	64.2	536	2 Q9PVD3	Q9PVD3 brachydanio
12	1151	50.4	542	2 Q9PVD2	Q9PVD2 brachydanio
13	1078	47.2	575	2 Q9PWB7	Q9PWB7 brachydanio
14	1050.5	46.0	550	1 PRRR_HUMAN	P49190 homo sapien
15	1011.5	44.3	546	1 PRRR_RAT	P70555 rattus norv
16	1006.5	44.1	546	1 PRRR_MOUSE	Q91V95 mus musculu
17	991	43.4	589	2 Q9GMD1	Q9GMD1 oryctolagus
18	777	34.0	147	2 Q76N28	Q76N28 rattus norv
19	776	34.0	459	1 VIPR_MOUSE	P97751 mus musculu
20	773.5	33.9	444	2 Q9YHC6	Q9YHC6 rana ridibu
21	772	33.8	459	1 VIPR_RAT	P30083 rattus norv
22	762.5	33.4	458	1 VIPR_PIG	Q28992 sus scrofa
23	757.5	33.2	449	1 SCRC_RAT	P23811 rattus norv
24	752.5	33.0	457	1 VIPR_HUMAN	P32241 homo sapien
25	749.5	32.8	445	1 SCRC_RABIT	O46502 oryctolagus
26	747	32.7	440	1 SCRC_HUMAN	P47872 homo sapien
27	746.5	32.7	457	2 Q6P2M6	Q6P2M6 homo sapien
28	746	32.7	440	2 Q81V17	Q81V17 homo sapien
29	743	32.5	419	2 Q8AXV4	Q8AXV4 fugu rubrip
30	729	31.9	457	1 VIPR_MELGA	Q91085 meleagris g
31	728	31.9	419	2 Q8AXV3	Q8AXV3 fugu rubrip

32	725	31.8	418	2 Q9IBG2	Q9IBG2 gallus gall
33	718	31.4	447	1 VIPR_CARAU	Q90308 carassius a
34	698	30.6	465	2 Q73769	Q73769 carassius a
35	687	30.1	468	1 PACR_HUMAN	P41586 homo sapien
36	683	29.9	435	2 Q64FL3	Q64FL3 oncorhynch
37	681.5	29.9	437	2 Q6PRD2	Q6PRD2 cavia porce
38	681.5	29.9	437	2 Q6PRD3	Q6PRD3 cavia porce
39	680	29.8	459	2 Q8BGA4	Q8BGA4 m mus muscu
40	680	29.8	465	2 Q9PTK1	Q9PTK1 xenopus lae
41	680	29.8	468	2 Q6NXJ9	Q6NXJ9 mus musculu
42	679	29.7	457	2 Q64FL5	Q64FL5 oncorhynch
43	676.5	29.6	437	1 VIPS_MOUSE	P41588 mus musculu
44	674	29.5	455	2 Q90Y10	Q90Y10 rana ridibu
45	672.5	29.5	437	1 VIPS_RAT	P35000 rattus norv

ALIGNMENTS

RESULT 1

ID	PTRR_RAT	STANDARD;	PTRR;	591 AA.
AC	P25961;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Parathyroid hormone/parathyroid hormone-related peptide receptor			
DE	precursor (PTH/PTHr receptor) (PTH/PTHr-P type I receptor).			
GN	Name=PTHr1; Synonyms=PTHr;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone;			
RX	MEDLINE=92212903; PubMed=1313566;			
RA	Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,			
RA	Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,			
RA	Kronenberg H.M., Segre G.V.;			
RT	"Expression cloning of a common receptor for parathyroid hormone and			
RT	parathyroid hormone-related peptide from rat osteoblast-like cells: a			
RT	single receptor stimulates intracellular accumulation of both cAMP and			
RL	inositol triphosphates and increases intracellular free calcium.";			
RN	Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94292182; PubMed=8020952;			
RA	Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F.,			
RA	Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;			
RT	"Cloning of a parathyroid hormone/parathyroid hormone-related peptide			
RT	receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line:			
RT	chromosomal assignment of the gene in the human, mouse, and rat			
RT	genomes.";			
RL	Genomics 20:20-26(1994).			

CC -1- FUNCTION: This is a receptor for parathyroid hormone and for
parathyroid hormone-related peptide. The activity of this receptor
is mediated by g proteins which activate adenyl cyclase and also
a phosphatidylinositol-calcium second messenger system.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).

CC -----
CC EMBL; M77184; AAA41811.1; -;

CC EMBL; L19475; AAA68098.1; -;

CC PIR; I54195; I54195.

DR HSSP; Q03431; IBL1.
DR RGD; 3442; Pthr1.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
DR G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
KW SIGNAL 1
FT CHAIN 27 591
FT
FT
FT DOMAIN 27 188
FT TRANSMEM 189 212
FT DOMAIN 213 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
FT DOMAIN 343 361
FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 591
FT DISULFID 48 117
FT DISULFID 108 148
FT DISULFID 131 170
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT CARBOHYD 166 166
FT CARBOHYD 176 176
SQ SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;
Query Match 95.8%; Score 2187; DB 1; Length 591;
Best Local Similarity 73.4%; Pred. No. 2.3e-156;
Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSSAYALVDDVFTKEEQIFLLHRAQAQCKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTASTSGPKRKEKASGKFPYPSKENKENVPTGSRRRGRPCLPENDNIVCWPL 120
Qy 26 ----- 25
Db 121 GAGEVAVPCPDYIDFNHKGHAYRCDRNGSEVVPVGHNRWTWANYSECLKFMTNETRE 180
Qy 26 -EVPDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYYIHMHPLSPMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYYIHMHPLSPMLRAASIFVK 240
Qy 85 DAVLYSGFTIDEARLTDEELHIIAQVPPPPAAAGVACRVAVTPFLFLATNYYWIL 144
Db 241 DAVLYSGFTIDEARLTDEELHIIAQVPPPPAAAGVACRVAVTPFLFLATNYYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGTFIFGWLGPVAVFVAVGVVRATLANTCWDLSGSHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGTFIFGWLGPVAVFVAVGVVRATLANTCWDLSGSHKK 360
Qy 205 WIQVPIIASVNLNFIILINIRVLATKLRETNAGRCDTTQQRKLLRSLVLVPLPGVH 264
Db 361 WIQVPIIASVNLNFIILINIRVLATKLRETNAGRCDTTQQRKLLRSLVLVPLPGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILYFCNGEVOAEIRKMSRWTLA 324

Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILYFCNGEVOAEIRKMSRWTLA 480
Qy 325 LDFKFKARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATNGHSQLPGHAKPG 384
Db 481 LDFKFKARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATNGHSQLPGHAKPG 540
Qy 385 APATETETLPVTMAVPKDDGFLNGSCGLDEERASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPVTMAVPKDDGFLNGSCGLDEERASGSARPPPLLOEGWETVM 591
RESULT 2
Q80WU8 PRELIMINARY; PRT; 591 AA.
ID Q80WU8
AC Q80WU8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor 1.
GN NamesPthr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051981; AAH51981.1; -.
DR HSSP; Q03431; IBL1.
DR MGD; MGI:97801; Pthr1.
DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
DR GO; GO:0030282; P:bone mineralization; IMP.
DR GO; GO:0001501; P:skeletal development; IMP.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.


```
SQ SEQUENCE 591 AA; 66371 MW; C2E6CAP2ABAFEEF CRC64;
Query Match 94.4%; Score 2156; DB 2; Length 591;
Best Local Similarity 72.4%; Pred. No. 5e-154;
Matches 428; Conservative 1; Mismatches 6; Indels 156; Gaps 1;

Qy 1 MGARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPSLALLCCPVLSAYALVDADDVFTKEQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTGPASTSGKPRKEKAPKFPYPSKENKDVPTGSRRRGRPCLPEDWNIVCWPL 120
Qy 26 ----- 25
Db 121 GAGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSMEVVPVGNHRTWANYSECLKFWNTRE 180
Qy 26 -EVFDRLGMIYTVGYSMASLASLTAVALLAYFRRLHCTRNYYIHMHFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLASLTAVALLAYFRRLHCTRNYYIHMHFSLFMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGVACRVAVTFFFLATNYYWIL 144
Db 241 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGVACRVAVTFFFLATNYYWIL 300
Qy 145 VEGYLHSLIFMAFPSEKKYLMGFTIFGWLPAVFVAVVGVVATLANTCWDLSGHHK 204
Db 301 VEGYLHSLIFMAFPSEKKYLMGFTIFGWLPAVFVAVVGVVATLANTCWDLSGHHK 360
Qy 205 WIQVPIASVVLNFIINIRVATKLRETNAGRCDTQQYRKLRLSTLVLVPLFGVH 264
Db 361 WIQVPIASVVLNFIINIRVATKLRETNAGRCDTQQYRKLRLSTLVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLQIQMHYEMLFNSQGFVAILIYFCNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMALPYTEVSGTLQIQMHYEMLFNSQGFVAILIYFCNGEVOAEIRKSWRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSLPRLPATNGHSQLPGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSLPRLPATNGHSQLPGHAKPG 540

RESULT 3
Q91WV4 ID Q91WV4 PRELIMINARY; PRT; 591 AA.
AC Q91WV4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor 1.
GN Name=Pthr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
```


Qy 385 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLQLQEGWETVM 435
Db 541 APAIENETIPVTMTVPKDDGFLNGSCGLDEASGSARPPPLQLQERWETVM 591

RESULT 5
PTRR HUMAN
ID PTHR_HUMAN STANDARD; PRT; 593 AA.
AC Q03431;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTH/PTHrP receptor) (PTH/PTHrP type I receptor).
GN Name=PTHr1; Synonyms=PTHr;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93238641; PubMed=8386612; DOI=10.1210/en.132.5.2157;
RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Jueppner H.;
RT "Identical complementary deoxyribonucleic acids encode a human renal
RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
RL Endocrinology 132:2157-2165(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93387403; PubMed=8397094; DOI=10.1016/0922-4106(93)90092-N;
RA Schneider H., Feyen J.-H., Rao Movva N.;
RT "Cloning and functional expression of a human parathyroid hormone
RT receptor.";
RL Eur. J. Pharmacol. 246:149-155(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95263723; PubMed=7745008; DOI=10.1210/jc.80.5.1611;
RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,
RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Jueppner H.;
RT "Pseudohypoparathyroidism type II is not caused by mutations in the
RT coding exons of the human parathyroid hormone (PTH)/PTH-related
RT peptide receptor gene.";
RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Levine M.A.;
RT "Characterization of cDNA and genomic DNA encoding the human PTH/PTHrP
RT receptor.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [5]
RP EXTRACELLULAR DOMAIN DISULFIDE BONDS.
RX MEDLINE=20374568; PubMed=10913300; DOI=10.1021/bi0001426;
RA Grauschopf U., Lillie H., Honold K., Wozny M., Reusch D., Esswein A.,
RA Schafer W., Rucknagel K.P., Rudolph R.;
RT "The N-terminal fragment of human parathyroid hormone receptor 1
RT constitutes a hormone binding domain and reveals a distinct disulfide
RT pattern.";
RL Biochemistry 39:8878-8887(2000).
RN [6]
RP STRUCTURE BY NMR OF 169-198
RX MEDLINE=98409426; PubMed=9737850; DOI=10.1021/bi981265h;
RA Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
RT "Binding domain of human parathyroid hormone receptor: from
RT conformation to function.";
RL Biochemistry 37:12737-12743(1998).
RN [7]
RP VARIANT JMC ARG-223.
RX MEDLINE=95215874; PubMed=7701349;

RA Schipani E., Kruse K., Jueppner H.;
RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
RT metaphyseal chondrodysplasia.";
RL Science 268:98-100(1995).
RN [8]
RP VARIANTS JMC ARG-223 AND PRO-410.
RX MEDLINE=96366745; PubMed=8703170; DOI=10.1056/NEJM199609053351004;
RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
RA Kooh S.W., Cole W.G., Jueppner H.;
RT "Constitutively activated receptors for parathyroid hormone and
RT parathyroid hormone-related peptide in Jansen's metaphyseal
RT chondrodysplasia.";
RL N. Engl. J. Med. 335:708-714(1996).
RN [9]
RP CHARACTERIZATION OF VARIANTS JMC ARG-223 AND PRO-410.
RX MEDLINE=97322091; PubMed=9178745; DOI=10.1210/me.11.7.851;
RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
RA Jueppner H.;
RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
RT receptors mutated at the two loci for Jansen's metaphyseal
RT chondrodysplasia.";
RL Mol. Endocrinol. 11:851-858(1997).
RN [10]
RP VARIANT BOD LEU-132.
RX MEDLINE=98417978; PubMed=9745456; DOI=10.1210/jc.83.9.3373;
RA Zhang P., Jobert A.-S., Couvineau A., Silve C.;
RT "A homozygous inactivating mutation in the parathyroid
RT hormone/parathyroid hormone-related peptide receptor causing
RT Blomstrand chondrodysplasia.";
RL J. Clin. Endocrinol. Metab. 83:3365-3368(1998).
RN [11]
RP VARIANT JMC ARG-458.
RX MEDLINE=99415605; PubMed=10487664; DOI=10.1210/jc.84.9.3052;
RA Schipani E., Langman C.B., Hunzelman J., Le Merrier M., Loke K.Y.,
RA Dillon M.J., Silve C., Jueppner H.;
RT "A novel parathyroid hormone (PTH)/PTH-related peptide receptor
RT mutation in Jansen's metaphyseal chondrodysplasia.";
RL J. Clin. Endocrinol. Metab. 84:3052-3057(1999).
RN [12]
RP VARIANT ENCHONDROMATOSIS CVS-150.
RX MEDLINE=21918585; PubMed=11850620; DOI=10.1038/ng844;
RA Hopyan S., Gokgoz N., Poon R., Gensure R.C., Yu C., Cole W.G.,
RA Bell R.S., Jueppner H., Andrusis I.L., Wunder J.S., Alman B.A.;
RT "A mutant PTH/PTHrP type I receptor in enchondromatosis.";
RL Nat. Genet. 30:306-310(2002).
RN [13]
RP FUNCTION: This is a receptor for parathyroid hormone and for
RP parathyroid hormone-related peptide. The activity of this receptor
RP is mediated by G proteins which activate adenylyl cyclase and also
RP a phosphatidylinositol-calcium second messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in most tissues. Most abundant in
CC kidney, bone and liver.
CC -1- DISEASE: Defects in PTHr1 are the cause of Jansen's metaphyseal
CC chondrodysplasia (JMC) [MIM:158400]. JMC is a rare autosomal
CC dominant disorder characterized by a short-limbed dwarfism
CC associated with hypercalcemia and normal or low serum
CC concentrations of the two parathyroid hormones.
CC -1- DISEASE: Defects in PTHr1 are the cause of chondrodysplasia
CC Blomstrand type (BOCD) [MIM:215045]. BOCD is a severe skeletal
CC dysplasia.
CC -1- DISEASE: Defects in PTHr1 can be a cause of enchondromatosis
CC [MIM:166000]. Enchondromas are common benign cartilage tumors of
CC bone. They can occur as solitary lesions or as multiple lesions in
CC enchondromatosis (Ollier and Maffucci diseases). Clinical problems
CC caused by enchondromas include skeletal deformity and the
CC potential for malignant change to osteosarcoma.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; L04308; AAA36525.1; -;
 DR EMBL; X68596; CAA48589.1; -;
 DR EMBL; U22409; AAB60657.1; -;
 DR EMBL; U22401; AAB60657.1; JOINED.
 DR EMBL; U22402; AAB60657.1; JOINED.
 DR EMBL; U22403; AAB60657.1; JOINED.
 DR EMBL; U22404; AAB60657.1; JOINED.
 DR EMBL; U22405; AAB60657.1; JOINED.
 DR EMBL; U22406; AAB60657.1; JOINED.
 DR EMBL; U22407; AAB60657.1; JOINED.
 DR EMBL; U22408; AAB60657.1; JOINED.
 DR EMBL; U17418; AAA56774.1; -;
 DR PIR; I38139; A49191.
 DR PDB; 1BLJ; NMR; @=168-198.
 DR PDB; 1ET2; Model; S=168-469.
 DR PDB; 1ET3; Model; S=168-469.
 DR Genew; HGNC:9608; PTHR1.
 DR MIM; 168468; -;
 DR MIM; 156400; -;
 DR MIM; 215045; -;
 DR MIM; 166000; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
 DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; GPCRSECRETIN.
 DR SMART; SMW0008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 DR 3D-structure; Disease mutation; Dwarfism; G-protein coupled receptor;
 KW Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 593 Parathyroid hormone/parathyroid hormone-
 FT related peptide receptor.
 FT DOMAIN 27 188 Extracellular (Potential).
 FT TRANSMEM 189 212 1 (Potential).
 FT DOMAIN 213 219 Cytoplasmic (Potential).
 FT TRANSMEM 220 239 2 (Potential).
 FT DOMAIN 240 282 Extracellular (Potential).
 FT TRANSMEM 283 306 3 (Potential).
 FT DOMAIN 307 320 Cytoplasmic (Potential).
 FT TRANSMEM 321 342 4 (Potential).
 FT DOMAIN 343 361 Extracellular (Potential).
 FT TRANSMEM 362 382 5 (Potential).
 FT DOMAIN 383 409 Cytoplasmic (Potential).
 FT TRANSMEM 410 428 6 (Potential).
 FT DOMAIN 429 440 Extracellular (Potential).
 FT TRANSMEM 441 463 7 (Potential).
 FT DOMAIN 464 593 Cytoplasmic (Potential).

Query Match 88.0%; Score 2008; DB 1; Length 593;
 Best Local Similarity 67.3%; Pred. No. 7.1e-143;
 Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSLALLCCPVLSSAVAL----- 25

Db 1 MGTARIAPGLALLCCPVLSSAVALVDVDDVMTKEQIFLLHRAQAQCKRLKEVLQRP 60

QY 26 ----- 25

Db 61 SIMESDKGWTSASTSGKPRDKASGLYPESEDKAPTGSRYGRPCLPWDHILCWPL 120

QY 26 ----- 25
 Db 121 GAGEVAVPCDDYIYDFNHKGHAYRRCDBNGSWELVPGHNRWTWYSECVKLTNETRE 180
 QY 26 -EVFDRGLMIYTVGYSGMSLASLTVAVLILAYFRRLHCTTRNYIHHMFLSFMRLAAASIFVK 84
 Db 181 REVFDRLGMIYTVGYSVSLASLTVAVLILAYFRRLHCTTRNYIHHMFLSFMRLAAASIFVK 240
 QY 85 DAVLYSGFTLDEAERLTELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYYWIL 144
 Db 241 DAVLYSGATLDEAERLTELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYYWIL 300
 QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTTFGMGLPAVFVAVMVGVVRATLANTCWDLSGSHKK 204
 Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTTFGMGLPAVFVAVMVGVVRATLANTCWDLSGSHKK 360
 QY 205 WIIQVPIASVILNFIILFINIIRVLATKLRETNAGRCDTQQYRKLRLSTLVLVPLFGVH 264
 Db 361 WIIQVPIASVILNFIILFINIIRVLATKLRETNAGRCDTQQYRKLRLSTLVLVPLFGVH 420
 QY 265 YTVFMALPYTEVSGTLMQIMHYEMLFNSFGQFFVAILIYFCNGEVOAEIKKSWSRWTLA 324
 Db 421 YIVFMATPYTEVSGTLMQIMHYEMLFNSFGQFFVAILIYFCNGEVOAEIKKSWSRWTLA 480
 QY 325 LDFKRRKARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSOLPGHAKP 383
 Db 481 LDFKRRKARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSOLPGHAKP 540
 QY 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSRAPPLLOQMETVM 435
 Db 541 GTPALETLETPPMAAAPKDDGFLNGSCGLDEASGSRAPPLLOQMETVM 593

RESULT 6

Q9TU31 PRELIMINARY; PRT; 595 AA.
 ID Q9TU31
 AC Q9TU31;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Parathyroid hormone receptor-1.
 GN Name=PTH1;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF167095; AAD55938.1; -;
 DR HSSP; Q03431; 1BLI.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
 DR GO; GO:0004931; F:parathyroid hormone receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR InterPro; IPR002170; Phrmn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PRINTS; PR00393; PTRHORMONER.
 DR SMART; SMW0008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match 85.78; Score 1957; DB 2; Length 595;
Best Local Similarity 65.61; Pred. No. 4.9e-139;
Matches 394; Conservative 11; Mismatches 24; Indels 172; Gaps 5;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPGLALLCCPVLSSAYALVDADDVMTKEBQIFLLHRAQAQCKRLKEVLQRP 60
QY 26 ----- 25
Db 61 DIMESDKGASASTSGPKKKEKAGSLYPESEEDKEVPTGSRHGRPCLPEDWHILCWPL 120
QY 26 ----- 25
Db 121 GAGEVVAVPCPDYIYDFNHKGHAYRCDRNGSWELVPGHNRWTANYSECVKELTNETRE 180
QY 26 -EYFDRGLMIYTVGYSMASLASLTAVLILAYFRRLHCTRYNIHMHPLSLMPLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRYNIHMHPLSLMPLRAVSIFVK 240
QY 85 DAVLYSGFTLDEARLTELLEELHIIAQVPPPPAAAAGYACRVAVTFFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTELLEELRAIAQAAPPPTAAA-GYACRVAVTFFFLYFLATNYWIL 299
QY 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFVAVVGVVRATLANTCGDLSGHHK 204
Db 300 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFVAVVGVVRATLANTCGDLSGHHK 359
QY 205 WIIQVPLASVNLFLFINIRVLATKLRNAGCDTRQQRKLLRSTLVLPVFGVH 264
Db 360 WIIQVPLASVNLFLFINIRVLATKLRNAGCDTRQQRKLLRSTLVLPVFGVH 419
QY 265 YTVFMALPYTEVSGTLQWQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 324
Db 420 YIVFMATPYTEVSGTLQWQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 479
QY 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSRPLP-----ATTNGHSOL 377
Db 480 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSRPLPAAAAATTATTNGHPPI 539
QY 378 PGHAKGAPATETETLPVT---NAVPKDGDGLNGSCGLDEEASGAPRPPALLQEWETV 434
Db 540 PGHTKGPAP-----TLPTATPPATAAPKDDGLNGSCGLDEEASAPRPPALLQEWETV 594
QY 435 M 435
Db 595 M 595

RESULT 7
Q7YRI3
ID Q7YRI3 PRELIMINARY; PRT; 599 AA.
AC Q7YRI3
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Parathyroid hormone/parathyroid hormone related protein receptor.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu H., Barling P.M., Ma L., Nicholson L.F.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY328401; AAP93208.1; -
DR HSSP; Q03431; 1BL1.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004930; F-G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.

DR Pfam; PF000002; 7tm.2; 1.
DR Pfam; PF02793; HRM; 1.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G PROTEIN RECP F2_1; 1.
DR PROSITE; PS0227; G PROTEIN RECP F2_3; 1.
DR PROSITE; PS0261; G PROTEIN RECP F2_4; 1.
KW Receptor.
SQ SEQUENCE. 589 AA; 65733 MW; 08A0577FB042A77A CRC64;

Query Match 84.61; Score 1932; DB 2; Length 589;
Best Local Similarity 65.21; Pred. No. 3.7e-137;
Matches 386; Conservative 15; Mismatches 31; Indels 160; Gaps 4;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPGLALLCCPVLSSAYALVDADDVMTKEBQIFLLHRAQAQCKRLKEVLQRP 60
QY 26 ----- 25
Db 61 DIMESDKGASASTSGPKKKEKAGSLYPESEEDKEVPTGSRHGRPCLPEDWHILCWPM 120
QY 26 ----- 25
Db 121 GAGEVVAVPCPDYIYDFNHKGHAYRCDRNGSWELVPGHNRWTANYSECVKELTNETRE 180
QY 26 -EYFDRGLMIYTVGYSMASLASLTAVLILAYFRRLHCTRYNIHMHPLSLMPLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRYNIHMHPLSLMPLRAVSIFVK 240
QY 85 DAVLYSGFTLDEARLTELLEELHIIAQVPPPPAAAAGYACRVAVTFFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTELLEELRAIAQAAPPPTAAA-GYVGRVAVTFFFLYFLATNYWIL 299
QY 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFVAVVGVVRATLANTCGDLSGHHK 204
Db 300 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFVAVVGVVRATLANTCGDLSGHHK 359
QY 205 WIIQVPLASVNLFLFINIRVLATKLRNAGCDTRQQRKLLRSTLVLPVFGVH 264
Db 360 WIIQVPLASVNLFLFINIRVLATKLRNAGCDTRQQRKLLRSTLVLPVFGVH 419
QY 265 YTVFMALPYTEVSGTLQWQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 324
Db 420 YIVFMATPYTEVSGTLQWQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 479
QY 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSRP-LPPATTNGHSGLPGHAKP 383
Db 480 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSRP-LPPATTNGHSGLPGHAKP 539
QY 384 GAPATETETLPVTMAYPKDDGLNGSCGLDEEASGAPRPPALLQEWETVM 435
Db 540 GSPA--LQATPPAATAAPKDDGLNGSCGLDEEACAPRPPVLLQEWETVM 589

RESULT 8
P7RR_PIG
ID P7RR_PIG STANDARD; PRT; 585 AA.
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).
GN Name=PTHr1; Synonyms=PTHr;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305358; PubMed=8688470; DOI=10.1016/0167-4781(96)00035-8;
RA Black E.C., Smith D.P., Zhang X.Y., Frolík C.A., Harvey A.,
ChandraSekhar S., Hsiung H.M.;

"Structure and functional expression of a complementary DNA for porcine parathyroid hormone/parathyroid hormone-related peptide receptor";
 RL Biochim. Biophys. Acta 1307:339-347(1996).
 CC -1- FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase and also a phosphatidylinositol-calcium second messenger system (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U18315; AAC48619.1; -.
 DR HSSP; Q03431; 1BL1.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm2; 1.
 DR Pfam; PF02793; HRM1; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS00651; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS00652; G_PROTEIN_RECP_F2_4; 1.
 DR PROSITE; PS00653; G_PROTEIN_RECP_F2_5; 1.
 KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 585 Parathyroid hormone/parathyroid hormone-related peptide receptor.
 FT DOMAIN 27 184 Extracellular (Potential).
 FT TRANSMEM 185 208 1 (Potential).
 FT DOMAIN 209 215 Cytoplasmic (Potential).
 FT TRANSMEM 216 235 Extracellular (Potential).
 FT DOMAIN 236 277 Extracellular (Potential).
 FT TRANSMEM 278 301 Cytoplasmic (Potential).
 FT DOMAIN 302 315 4 (Potential).
 FT TRANSMEM 316 337 Extracellular (Potential).
 FT DOMAIN 338 356 Extracellular (Potential).
 FT TRANSMEM 357 377 Cytoplasmic (Potential).
 FT DOMAIN 378 404 Cytoplasmic (Potential).
 FT TRANSMEM 405 423 Extracellular (Potential).
 FT DOMAIN 424 435 Extracellular (Potential).
 FT TRANSMEM 436 458 Cytoplasmic (Potential).
 FT DOMAIN 459 585 By similarity.
 FT DISULFID 48 113 By similarity.
 FT DISULFID 104 144 By similarity.
 FT DISULFID 127 166 By similarity.
 FT CARBOHYD 147 157 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 157 171 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 162 172 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;
 Query Match 84.3%; Score 1925; DB 1; Length 585;
 Best Local Similarity 65.6%; Pred. No. 1.2e-136;
 Matches 386; Conservative 13; Mismatches 33; Indels 156; Gaps 4;
 QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
 DB 1 MGAARIAPGLALLCCPVLSSAYALVDDDMVTKEQIFLLHRAQAQCKRLKEVLQRP 60
 QY 26 ----- 25
 DB 61 DIMESDKGWSAAPTSGKPRKEKASGLKYPESGEDTSGRQPCLPEDWHLCWPLGAPG 120
 QY 26 -----EVF 28

121 EVVAMPCPDYIYDFNHKHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNETREVEF 180
 QY 29 DRIGMTYTVGYSSMSLASLTVAVLILAYFRRLHCTRYIHHMFSLPMLRAASIFVKDAVL 88
 DB 181 DRIGMTYTVGYSSMSLASLTVAVLILAYFRRLHCTRYIHHMFSLPMLRAASIFVKDAVL 240
 QY 89 YSGFTLDEAERLTERELHIIAQVPPPPAAAAGYACRVAATFELFLATNYWILVEGL 148
 DB 241 YSGATLDEAERLTERELHIIAQVPPPPAAAAGYACRVAATFELFLATNYWILVEGL 239
 QY 149 YLHSLIFMAFFSEKKYKLGFTFGWGLPAFVAVVWVGVRAATLANTCGWLSGSHKWIQ 208
 DB 300 YLHSLIFMAFFSEKKYKLGFTFGWGLPAFVAVVWVGVRAATLANTCGWLSGSHKWIQ 359
 QY 209 VPIASVVLNFIPIINIRVLATKLRETNAGRCDTQOYKRLRLTLVPLFGVHYTVF 268
 DB 360 VPIASVVLNFIPIINIRVLATKLRETNAGRCDTQOYKRLRLTLVPLFGVHYTVF 419
 QY 269 MALPYTEVSGTLQIQMHYEMLFNSFGPFVLIYCFNGEVOAEIRKWSRWTLALDFK 328
 DB 420 MATPYTEVSGTLQIQMHYEMLFNSFGPFVLIYCFNGEVOAEIRKWSRWTLALDFK 479
 QY 329 RKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATNGHSQLPGHAKPGAPA 387
 DB 480 RKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATNGHSQLPGHAKPGAPA 539
 QY 388 TETETLPVTMAVPKDQDGLNGSCGDLDEASGASRPPILQEGWETVM 435
 DB 540 --LQTTTPVVAAPKDDGFLNGSCGDLDEASGASRPPILQEGWETVM 585
 RESULT 9
 PTHR_DIDMA STANDARD; PRT; 585 AA.
 AC P25107;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHrP type I receptor).
 GN Names: PTHrP; Synonyms: PTHrP;
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92054592; PubMed=1658941;
 RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E.,
 RA Richards J., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr.,
 RA Kronenberg H.M., Segre G.V.;
 RT "A G protein-linked receptor for parathyroid hormone and parathyroid hormone-related peptide";
 RL Science 254:1024-1026(1991).
 CC -1- FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase and also a phosphatidylinositol-calcium second messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M74445; AAA30979.1; -.
 DR PIR; A39286; A39286.
 DR HSSP; Q03431; 1BL1.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 06:12:59 ; Search time 84 Seconds
(without alignments)
2002.866 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 435

Sequence: 1 MGARIAPSLALLCCPVLS.....EASGSARPPPLQGGWETVM 435

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	3 AAB07529	Aab07529 A mutant
2	410	94.3	446	3 AAY96983	Aay96983 Tethered
3	410	94.3	591	2 AAR92277	Aar92277 Rat bone
4	410	94.3	591	2 AAW73316	Aaw73316 Parathyro
5	410	94.3	591	8 ADH61247	Adh61247 Rat bone
6	404	92.9	591	7 ADE83416	Ade83416 Rat Prote
7	324	74.5	324	3 AAY96985	Aay96985 Tethered
8	318	73.1	591	8 ADO29629	Ado29629 Mouse GPC
9	309	71.0	591	2 AAR27706	Aar27706 Rat bone
10	299	68.7	335	3 AAY96984	Aay96984 Tethered
11	49	11.3	435	3 AAY96987	Aay96987 Human tet
12	49	11.3	448	3 AAY96986	Aay96986 Human tet
13	49	11.3	450	3 AAY96988	Aay96988 Human tet
14	49	11.3	593	2 AAW73317	Aaw73317 Human par
15	49	11.3	593	4 ABB56385	Abb56385 Non-endog
16	49	11.3	593	4 AAB71876	Aab71876 Human PTR
17	49	11.3	593	6 ABP81872	Abp81872 Human par
18	49	11.3	593	7 ADE83418	Ade83418 Human pro
19	49	11.3	593	7 ADF70390	Adf70390 Human PTH
20	49	11.3	593	8 ADH61248	Adh61248 Human PTH
21	49	11.3	593	8 ADO29628	Ado29628 Human GPC
22	49	11.3	593	8 ADO18189	Ado18189 Human sof
23	49	11.3	593	8 ADQ76825	Adq76825 Human wil
24	49	11.3	593	8 ADR47544	Adr47544 Human par
25	49	11.3	595	6 ABG73825	Abg73825 Canine pa

26	49	11.3	614	2 AAR27707	Aar27707 Human kid
27	49	11.3	975	8 ADQ76835	Adq76835 Parathyro
28	43	9.9	964	7 ADC86169	Adc86169 Human GPC
29	40	9.2	129	8 ADQ76849	Adq76849 Human par
30	40	9.2	289	8 ADQ76854	Adq76854 Parathyro
31	40	9.2	325	8 ADQ76855	Adq76855 Parathyro
32	40	9.2	339	8 ADQ76856	Adq76856 Parathyro
33	40	9.2	354	8 ADQ76857	Adq76857 Parathyro
34	40	9.2	368	8 ADQ76858	Adq76858 Parathyro
35	34	7.8	34	6 ABR61989	AbR61989 Human par
36	34	7.8	515	2 AAR27704	Aar27704 Opossum k
37	34	7.8	515	2 AAR92275	Aar92275 Opossum k
38	34	7.8	515	2 AAW73314	Aaw73314 Parathyro
39	34	7.8	515	8 ADH61245	Adh61245 Opossum k
40	34	7.8	585	2 AAR27705	Aar27705 Opossum k
41	34	7.8	585	2 AAR92276	Aar92276 Opossum k
42	34	7.8	585	2 AAW73315	Aaw73315 Parathyro
43	34	7.8	585	8 ADH61246	Adh61246 Opossum k
44	31	7.1	593	2 AAR92278	Aar92278 Human kid
45	29	6.7	275	8 ADQ76853	Adq76853 Parathyro

ALIGNMENTS

RESULT 1
AAB07529
ID AAB07529 standard; protein; 435 AA.

XX AAB07529;
AC AAB07529;
XX 20-OCT-2000 (first entry)
DT
XX
DE A mutant parathyroid hormone (PTH) receptor designated rdeltaNt.
XX
KW Mutant; parathyroid hormone; PTH; receptor; rdeltaNt;
KW ligand binding domain.
XX Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /note= "signal peptide"
FT /note= "mature protein"

XX WO200040698-A1.

XX 13-JUL-2000.

XX 31-DEC-1998; 98WO-US027862.

XX 31-DEC-1998; 98WO-US027862.

XX (GEMO) GEN HOSPITAL CORP.

XX Gardella TJ, Kronenberg HM, Potts JT;

XX WPI; 2000-465971/40.

XX N-PSDB; AAS58932.

XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity.

XX Claim 17; Fig 1; 81pp; English.

XX The present sequence represents a mutant parathyroid hormone (PTH) receptor, designated rdeltaNt. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists

```
CC and antagonists of PTH receptor activity
XX Sequence 435 AA;
SQ

Query Match 100.0%; Score 435; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGAARIAPSLALLCCPVLSSAYALEVDFRLGMIYTVGYSMASLSTVAVLILAYFRLH 60
Db 1 MGAARIAPSLALLCCPVLSSAYALEVDFRLGMIYTVGYSMASLSTVAVLILAYFRLH 60
Qy 61 CTRNYIHMHFLSMLRAASTFVKDAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAV 120
Db 61 CTRNYIHMHFLSMLRAASTFVKDAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAV 120
Qy 121 GYAGCRVAVTFYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFV 180
Db 121 GYAGCRVAVTFYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFV 180
Qy 181 AVWVGVRATLANTCCDWLSSGHKKWIIQVPIASVWLNFLFINIRVLATKLRETNAGR 240
Db 181 AVWVGVRATLANTCCDWLSSGHKKWIIQVPIASVWLNFLFINIRVLATKLRETNAGR 240
Qy 241 CDTROQYRKLLRSTLVLPVLFVGHYTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGQPFVA 300
Db 241 CDTROQYRKLLRSTLVLPVLFVGHYTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGQPFVA 300
Qy 301 IYFCNGEVAQAEIRKSWRWTALDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360
Db 301 IYFCNGEVAQAEIRKSWRWTALDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360
Qy 361 PLSRPLPATTNGHSQLPQHAKEGAPATETETLPTVMAVPKDDGFLNGSCGLDEEASGS 420
Db 361 PLSRPLPATTNGHSQLPQHAKEGAPATETETLPTVMAVPKDDGFLNGSCGLDEEASGS 420
Qy 421 ARPPPLLOEGWETVM 435
Db 421 ARPPPLLOEGWETVM 435

RESULT 2
AAY96983
ID AAY96983 standard; protein; 446 AA.
XX
AC AAY96983;
XX
DT 31-OCT-2000 (first entry)
XX
DE Tethered PTH-1 receptor, Tether1.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX
OS Rattus sp.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX Peptide /label= PTH-1_receptor_signal_sequence
XX Peptide 24..32
XX Peptide /label= PTH_residues_1-9
XX Peptide 33..36
XX Peptide /label= linker
XX Protein 37..446
XX /label= PTH-1_receptor
XX /note= "residue 182 to end"
XX
XX WO2000039278-A2.
XX
XX 06-JUL-2000.
PD
XX
```


PT Antibody to parathyroid hormone receptor - for diagnostic or therapeutic use.

XX Claim 6; Fig 3; 63pp; English.

PS This sequence represents the rat parathyroid hormone (PTH) receptor R15B, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia

XX Sequence 591 AA;

Query Match 94.3%; Score 410; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLGMIYTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 85
DB 182 EVFDRLGMIYTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 241

QY 86 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 145
DB 242 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 301

QY 146 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVAVVGRATLANTGCDLSSGHKKW 205
DB 302 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVAVVGRATLANTGCDLSSGHKKW 361

QY 206 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
DB 362 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 421

QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAIIFCNGEVAQAEIRKSNRWTLAL 325
DB 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAIIFCNGEVAQAEIRKSNRWTLAL 481

QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTTNGHSQLPCHAKPGA 385
DB 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTTNGHSQLPCHAKPGA 541

QY 386 PATETETLPVTMAVPKDDGFLNGSCGLDEEASGARPPPLQGGWETVM 435
DB 542 PATETETLPVTMAVPKDDGFLNGSCGLDEEASGARPPPLQGGWETVM 591

RESULT 5
ADH61247 standard; protein; 591 AA.

AC ADH61247;

XX 25-MAR-2004 (first entry)

XX Rat bone PTH/PTHrP receptor, R15B.

XX osteopathic; Parathyroid hormone receptor; hypercalcaemia;
XX hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
XX oesophagus multiple myeloma; hypocalcaemia; cytostatic; rat; PTH; PTHrP;
XX PTH-related protein; receptor.

XX Rattus rattus.

XX Key Location/Qualifiers
FH Region 193..211
FT /note= "Transmembrane region 1"
FT Region 222..240
FT /note= "Transmembrane region 2"
FT Region 300..316
FT /note= "Transmembrane region 3"
FT Region 326..342
FT /note= "Transmembrane region 4"

FT Region 365..383
FT /note= "Transmembrane region 5"
FT Region 409..428
FT /note= "Transmembrane region 6"
FT Region 445..463
FT /note= "Transmembrane region 7"

XX US2003153041-A1.
XX 14-AUG-2003.
XX 09-OCT-2002; 2002US-00267730.
XX 05-APR-1991; 91US-00681702.
XX 06-APR-1992; 92US-00864475.
XX 06-JUN-1995; 95US-00471494.
XX 24-NOV-1998; 98US-00199874.
XX (GEO) GEN HOSPITAL CORP.
XX Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potte JT;
PI Schipani E;
XX WPI; 2004-051107/05.
XX N-PSDB; ADH61258.
XX New isolated DNA encoding parathyroid hormone receptor polypeptides, useful for diagnosing and treating disorders associated with parathyroid hormone receptors, e.g. hypercalcaemia, osteoporosis or multiple myeloma.
XX Disclosure; SEQ ID NO 20; 71pp; English.
XX The invention relates to parathyroid hormone (PTH) receptor and its corresponding nucleic acid sequence. The parathyroid hormone receptor polypeptides, polynucleotides and antibodies are useful for diagnosing, prognosticating and treating disorders associated with parathyroid hormone receptors, e.g. hypercalcaemia, hyperparathyroidism, osteoporosis, carcinomas of the breast, lung and prostate, epidermoid cancers of the head and neck of the oesophagus, multiple myeloma, or hypocalcaemia. The DNAs and polypeptides are also useful for screening candidate compounds for antagonistic or agonistic effects on parathyroid hormone receptor activity. The compounds are also useful in manufacturing diagnostic agents used as diagnostic tools to diagnose hypercalcaemia and to distinguish between hypercalcaemic conditions. The present sequence is rat bone PTH/PTHrP (PTH-related protein) receptor protein.

XX Sequence 591 AA;

Query Match 94.3%; Score 410; DB 8; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLGMIYTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 85
DB 182 EVFDRLGMIYTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 241

QY 86 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 145
DB 242 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 301

QY 146 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVAVVGRATLANTGCDLSSGHKKW 205
DB 302 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVAVVGRATLANTGCDLSSGHKKW 361

QY 206 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
DB 362 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 421

QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAIIFCNGEVAQAEIRKSNRWTLAL 325
DB 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAIIFCNGEVAQAEIRKSNRWTLAL 481

QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTTNGHSQLPCHAKPGA 385

|||||
482 DFKKARSGSSSYSGPMVSHSTVTVNGPRAGLSPLSPRLPPATTNGHSQLPGHAKPGA 541
386 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOQGWETVM 435
542 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOQGWETVM 591
RESULT 6
ADE83416
ID ADE83416 standard; protein; 591 AA.
XX ADE83416;
AC ADE83416;
XX 29-JAN-2004 (first entry)
DT
XX Rat Protein P25961, SEQ ID NO 11011.
DE
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P25961.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 591 AA;
Query Match 92.9%; Score 404; DB 7; Length 591;
Best Local Similarity 100.0%; Pred No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRRLHCTRNYYHMHMFLSPMLRAASIFVKD 85
DB 182 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRRLHCTRNYYHMHMFLSPMLRAASIFVKD 241
QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYFLATNYYWILV 145
DB 242 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYFLATNYYWILV 301
QY 146 EGLYLSLIFMAFFSEKKYLGFTIFGWLPAVFAVWVGVRATLANTGWDLSGGHKKW 205
DB 302 EGLYLSLIFMAFFSEKKYLGFTIFGWLPAVFAVWVGVRATLANTGWDLSGGHKKW 361
QY 206 IIQVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
DB 362 IIQVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 421
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAVIYCFNGEVOAEIRKSWSRWTLAL 325
DB 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAVIYCFNGEVOAEIRKSWSRWTLAL 481
QY 326 DFKRKARSGSSSYSGPMVSHSTVTVNGPRAGLSPLSPRLPPATTNGHSQLPGHAKPGA 385
DB 482 DFKRKARSGSSSYSGPMVSHSTVTVNGPRAGLSPLSPRLPPATTNGHSQLPGHAKPGA 541
QY 386 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOQ 429
DB 542 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOQ 585
RESULT 7
AA996985
ID AA996985 standard; protein; 324 AA.
XX AA996985;
XX 19-DEC-2000 (first entry)
DT
XX Tethered PTH-1 receptor, r-del-Nt/Ct.
DE
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; r-delta-Nt/Ct; tethered receptor;
KW osteoporosis.
XX Rattus sp.
XX Synthetic.
XX Chimeric.
XX WO200039278-A2.
XX 06-JUL-2000.
XX 30-DEC-1999; 99WO-US031108.
XX 31-DEC-1998; 98US-0114577P.
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTI/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
DR N-PSDB; AAM51734.
XX
XX New compound comprising an amino terminal signaling functional domain

PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 22; Fig 10; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R₁-S-(L)_n-R or S-(L)_n-
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R₁ is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased bone activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTH-rP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 324 AA;

Query Match 74.5%; Score 324; DB 3; Length 324;
Best Local Similarity 100.0%; Pred. No. 3.6e-298;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGAARIAPSLALLCCPVLSAVALVFDRLGMIYTVGYSMASLTVAVLILAYFRLH 60
Db 1 MGAARIAPSLALLCCPVLSAVALVFDRLGMIYTVGYSMASLTVAVLILAYFRLH 60
Qy 61 CTRNYIHHMFLSMLRAASIFVKDVLVSGFTLDEAERLTEREELHIIAQQVPPPPAAA 120
Db 61 CTRNYIHHMFLSMLRAASIFVKDVLVSGFTLDEAERLTEREELHIIAQQVPPPPAAA 120
Qy 121 GYACRVAVFYFLATNYIIVLVEGLYLSLIFMAFFSEKKYKLGFTIFGWLPAVFV 180
Db 121 GYACRVAVFYFLATNYIIVLVEGLYLSLIFMAFFSEKKYKLGFTIFGWLPAVFV 180
Qy 181 AVWVGVRATLANTGCDLSSGKKWIIQVPLASVNLNFIINIRVLATKLRNAGR 240
Db 181 AVWVGVRATLANTGCDLSSGKKWIIQVPLASVNLNFIINIRVLATKLRNAGR 240
Qy 241 CDTQQVKRLRSFLVLPVLFVGHYTVFMAIPYEVSGTLWQIQMHYEMLFNSFGQFFVA 300
Db 241 CDTQQVKRLRSFLVLPVLFVGHYTVFMAIPYEVSGTLWQIQMHYEMLFNSFGQFFVA 300
Qy 301 IIVCFNGEVQAEIRKSWRWTLA 324
Db 301 IIVCFNGEVQAEIRKSWRWTLA 324

RESULT 8

AD029629

ID AD029629 standard; protein; 591 AA.

XX AC AD029629;

XX AC AD029629;

DT 29-JUL-2004 (first entry)

XX Mouse GPCR PTHR1, SEQ ID NO:731.

XX

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
KW cytosolic; antinflammatory; vasotropic; antidiarrhoeic; antidiabetic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;

KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
KW murine; receptor.
XX
OS Mus musculus.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li P;

XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

XX N-PSDB; ADO30323.

XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 151; SEQ ID NO 731; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 591 AA;

Query Match 73.1%; Score 318; DB 8; Length 591;

Best Local Similarity 100.0%; Pred. No. 3e-292;

Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EVFDRGLMIYTVGYSMASLTVAVLILAYFRLHCTRNVIHHMFLSMLRAASIFVKD 85

Db 182 EVFDRGLMIYTVGYSMASLTVAVLILAYFRLHCTRNVIHHMFLSMLRAASIFVKD 241

Qy 86 AVLVSFTLDEAERLTEREELHIIAQQVPPPPAAAAGVACRVAVTFFLYLATNYIWL 145

Db 242 AVLYSGFTLDEAEERLTHTEELHIIAQVPPPPAAAAAGVAGCRVAVTFFLYLATNYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVRAVATLANTGCDLSSGHKKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVRAVATLANTGCDLSSGHKKW 361
Qy 206 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCRDTQOQYRKLRLSTLVLPLFGVHY 265
Db 362 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCRDTQOQYRKLRLSTLVLPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVAILIYCFNGEVQAEIRKSWRWTAL 325
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVAILIYCFNGEVQAEIRKSWRWTAL 481
Qy 326 DFRRKARSGSSSYSGPM 343
Db 482 DFRRKARSGSSSYSGPM 499
RESULT 9
AAR27706
ID AAR27706 standard; protein; 591 AA.
XX AAR27706;
DT 25-MAR-2003 (revised)
DT 16-MAR-1993 (first entry)
XX
DE Rat bone PTH/PTHrP receptor clone R15B prod.
XX
KW Parathyroid hormone; related protein; calcium; antagonist; antibodies;
KW hypercalcaemia.
XX
OS Rattus rattus.
XX
PN WO9217602-A1.
XX
PD 15-OCT-1992.
XX
PF 06-APR-1992; 92WO-US002821.
XX
PR 05-APR-1991; 91US-00681702.
XX
PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX
PI Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
PI Schipani E;
XX
DR WPI; 1992-366271/44.
DR N-PSDB; AAQ29606.
XX
PT New DNA encoding parathyroid hormone receptor, DNA and antibodies - for
PT (differential) diagnosis of hypercalcaemia, and diagnosis and treatment
PT of tumours.
XX
XX Claim 20; Fig 3; 91pp; English.
XX
CC The rat bone parathyroid hormone/parathyroid hormone related protein
CC (PTH/PTHrP) receptor protein sequence was deduced from clone R15B obtd.
CC by screening a rat osteosarcoma (ROS) cell cDNA library to isolate those
CC expressing functionally intact PTH/PTHrP receptor proteins, performed
CC according to Gearing et al., (EMBO J. 8: 3676, 1989), by identifying
CC colonies capable of binding a suitable radio-labelled ligand. The
CC protein may be used in a therapeutic compen. to inhibit activation of PTH
CC or PTHrP and thus reduce the level of calcium in the blood. Cpds. capable
CC of competing with PTH or PTHrP for binding can be identified using the
CC protein and DNAs homologous to PTH DNA can be identified using fragments
CC of the clone as probes. The sequence may be used for the prodn. of
CC antibodies useful for the treatment, classification, prognosis and/or
CC treatment of disorders related to the interaction between a cell receptor
CC and a ligand such as in hypercalcaemia. See also AAR27704-16. (Updated on
CC 25-MAR-2003 to correct PN field.)

XX SQ Sequence 591 AA;
Query Match 71.0%; Score 309; DB 2; Length 591;
Best Local Similarity 99.8%; Pred. No. 1e-283;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 26 EVFDRGLMIYTVGYSMSLASLTAVAILAYFRRLHCTRNIIHMHMFLSPMLRAASIFVKD 85
Db 182 EVFDRGLMIYTVGYSMSLASLTAVAILAYFRRLHCTRNIIHMHMFLSPMLRAASIFVKD 241
Qy 86 AVLYSGFTLDEAEERLTHTEELHIIAQVPPPPAAAAAGVAGCRVAVTFFLYLATNYWILV 145
Db 242 AVLYSGFTLDEAEERLTHTEELHIIAQVPPPPAAAAAGVAGCRVAVTFFLYLATNYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVRAVATLANTGCDLSSGHKKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVRAVATLANTGCDLSSGHKKW 361
Qy 206 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCRDTQOQYRKLRLSTLVLPLFGVHY 265
Db 362 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCRDTQOQYRKLRLSTLVLPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVAILIYCFNGEVQAEIRKSWRWTAL 325
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVAILIYCFNGEVQAEIRKSWRWTAL 481
Qy 326 DFRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATNGHSQLPGHAKPGA 385
Db 482 DFRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATNGHSQLPGHAKPGA 541
Qy 386 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435
Db 542 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 591
RESULT 10
AAY96984
ID AAY96984 standard; protein; 335 AA.
XX AAY96984;
XX
DT 31-OCT-2000 (first entry)
XX
DE Tethered PTH-1 receptor, TetheriC.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tetheriC; osteoporosis.
XX
OS Rattus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..23 /label= PTH-1_receptor_signal_sequence
FT Peptide 24..32 /label= PTH_residues_1-9
FT Peptide 33..36 /label= linker
FT Protein 37..335 /label= PTH-1_receptor
FT /note= "residue 182 to 480"
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.

```

PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51733.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX
XX Claim 22; Fig 9; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases
XX and disorders associated with decreased tether1 activity, increasing cAMP
XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or
XX non-peptide PTH (claimed). The new compound can be administered by
XX inhalation unlike the large native PTH or PTHrP which avoids the need for
XX regular injections to treat osteoporosis
XX
XX Sequence 335 AA;
XX
Query Match 68.7%; Score 299; DB 3; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.9e-274;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 EVFDRLGMIYTVGYSMASLITVAVLLAYFRRLHCTRNVIHMHMFLSFMRLAASIFVKD 85
DB 37 EVFDRLGMIYTVGYSMASLITVAVLLAYFRRLHCTRNVIHMHMFLSFMRLAASIFVKD 96
QY 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAVGAGCRVAVTFPLYFLATNYYWILV 145
DB 97 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAVGAGCRVAVTFPLYFLATNYYWILV 156
QY 146 EGLYLHSLIFMAFSEKKYLWGFTIFCGGLPAVFAVWVGRATLANTGCWDLSSGHKKW 205
DB 157 EGLYLHSLIFMAFSEKKYLWGFTIFCGGLPAVFAVWVGRATLANTGCWDLSSGHKKW 216
QY 206 IIQVPILASVVLNFIPIRVLATKLRNTAGRCDTROQYRKLRLSTLVLVPLFGVHY 265
DB 217 IIQVPILASVVLNFIPIRVLATKLRNTAGRCDTROQYRKLRLSTLVLVPLFGVHY 276
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVAEIRKSWSRWTLA 324
DB 277 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVAEIRKSWSRWTLA 335

RESULT 11
AA96987
ID AAY96987 standard; protein; 435 AA.
XX
XX
AC AAY96987;
XX
XX 31-OCT-2000 (first entry)
XX
XX Human tethered PTH-1 receptor, hdelNT.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX
XX Homo sapiens.
XX Synthetic.
XX Chimeric.

```

```

XX PN WC200039278-A2.
XX PD 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51736.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX
XX Example 4; Fig 18; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases
XX and disorders associated with decreased tether1 activity, increasing cAMP
XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or
XX inhalation unlike the large native PTH or PTHrP which avoids the need for
XX regular injections to treat osteoporosis
XX
XX Sequence 435 AA;
XX
Query Match 11.3%; Score 49; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.4e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 121 GYAGCRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFSEKKYLGWFT 169
DB 119 GYAGCRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFSEKKYLGWFT 167

RESULT 12
AA96986
ID AAY96986 standard; protein; 448 AA.
XX
XX
AC AAY96986;
XX
XX 31-OCT-2000 (first entry)
XX
XX Human tethered PTH-1 receptor, Tether1.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX /label= Signal_sequence
XX /note= "Human PTH-1 receptor residues 1-23"
XX
XX Peptide 24..32

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 06:19:15 ; Search time 28 Seconds
(without alignments)
1159.727 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 435

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGARPPPLQEGWETVM 435

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgm2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410	94.3	591	2	US-08-468-249A-20
2	49	11.3	593	2	US-08-468-249A-21
3	49	11.3	593	4	US-09-631-603-21
4	49	11.3	593	4	US-09-826-509-563
5	48	11.0	207	4	US-08-811-519-31
6	34	7.8	515	2	US-08-468-249A-18
7	34	7.8	585	1	US-08-142-439A-6
8	34	7.8	585	2	US-08-142-551B-125
9	34	7.8	585	2	US-08-869-477-6
10	34	7.8	585	2	US-08-468-249A-19
11	31	7.1	593	3	US-08-468-011A-24
12	31	7.1	593	3	US-09-236-468A-24
13	29	6.7	52	3	US-08-468-011A-14
14	29	6.7	52	3	US-09-236-468A-14
15	28	6.4	536	4	US-09-449-632-2
16	25	5.7	60	3	US-08-468-011A-10
17	25	5.7	60	3	US-09-236-468A-10
18	25	5.7	575	4	US-09-449-632-5
19	24	5.5	25	1	US-07-864-475A-13
20	24	5.5	25	2	US-08-468-249A-13
21	24	5.5	26	1	US-07-864-475A-8
22	24	5.5	26	2	US-08-468-249A-8
23	19	4.4	19	1	US-07-864-475A-7
24	19	4.4	19	2	US-08-468-249A-7
25	18	4.1	19	1	US-07-864-475A-6
26	18	4.1	19	2	US-08-468-249A-6
27	18	4.1	60	3	US-08-468-011A-9

28 18 4.1 60 3 US-09-236-468A-9 Sequence 9, Appli
29 18 4.1 541 3 US-08-468-011A-2 Sequence 2, Appli
30 18 4.1 541 3 US-09-236-468A-2 Sequence 2, Appli
31 18 4.1 541 5 PCT-US95-07085-2 Sequence 2, Appli
32 18 4.1 542 4 US-09-449-632-4 Sequence 4, Appli
33 18 4.1 550 4 US-09-631-603-20 Sequence 20, Appli
34 18 4.1 550 4 US-09-826-509-565 Sequence 565, App
35 15 3.4 60 3 US-08-468-011A-19 Sequence 19, Appl
36 15 3.4 60 3 US-08-468-011A-20 Sequence 19, Appl
37 15 3.4 60 3 US-09-236-468A-19 Sequence 20, Appl
38 15 3.4 60 3 US-09-236-468A-20 Sequence 12, Appl
39 14 3.2 60 3 US-08-468-011A-12 Sequence 12, Appl
40 14 3.2 207 4 US-08-811-519-30 Sequence 30, Appl
41 14 3.2 440 4 US-09-631-603-22 Sequence 22, Appl
42 14 3.2 440 4 US-09-826-509-567 Sequence 567, App
43 14 3.2 449 1 US-08-142-439A-5 Sequence 5, Appli
44 14 3.2 449 2 US-08-869-477-5 Sequence 5, Appli
45 14 3.2 449 2 US-08-869-477-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-20

Query Match 94.3%; Score 410; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EVFRLGMIYTVGYSMISLASITVAVLILAYFRRRLHCTRNYYHMHFSLSEMLRAASIFVKD 85
Db 182 EVFRLGMIYTVGYSMISLASITVAVLILAYFRRRLHCTRNYYHMHFSLSEMLRAASIFVKD 241
Qy 86 AVLYSGFTLDEARLTDEEELHIIAQVPPPPAAAAAGVAGCRVAVTFFLYFLATNYYWILV 145
Db 242 AVLYSGFTLDEARLTDEEELHIIAQVPPPPAAAAAGVAGCRVAVTFFLYFLATNYYWILV 301
Qy 146 EGYLHLSLIFMAFSEKKYLMGFTIFGKGLPAVFAVAVVGVVATLANTGWDLSGGHKW 205
Db 302 EGYLHLSLIFMAFSEKKYLMGFTIFGKGLPAVFAVAVVGVVATLANTGWDLSGGHKW 361
Qy 206 IIQVPIIASVVLNFIILFNIIRVLATKLRNAGRCRDTQOYRKLRLSTLVLVPLFGVHY 265
Db 362 IIQVPIIASVVLNFIILFNIIRVLATKLRNAGRCRDTQOYRKLRLSTLVLVPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLWQIQHYEMLFNSFOGFFVAILIYFCNGEVQAEIRKSWSRWTLAL 325
Db 422 TVFMALPYTEVSGTLWQIQHYEMLFNSFOGFFVAILIYFCNGEVQAEIRKSWSRWTLAL 481
Qy 326 DFKKKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLPPATTNGHSQLPGHAKPGA 385
Db 482 DFKKKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLPPATTNGHSQLPGHAKPGA 541
Qy 386 PATETETLPVTMAYPKDDGFLNGSCGLDEEASGARPPPLLOQGWETVM 435
Db 542 PATETETLPVTMAYPKDDGFLNGSCGLDEEASGARPPPLLOQGWETVM 591

RESULT 2

US-08-468-249A-21

; Sequence 21, Application US/08468249A

; Patent No. 5886148

; GENERAL INFORMATION:

; APPLICANT: Segre et al., Gino V.

; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA

; TITLE OF INVENTION: ENCODING SAME

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,249A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/864,475

; FILING DATE: 06-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/681,702

; FILING DATE: 04-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 00786/071003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 593 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-468-249A-21

Query Match 11.3%; Score 49; DB 2; Length 593;

Best Local Similarity 100.0%; Pred. No. 4.4e-36;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHLSLIFMAFFSEKKYLMGFT 169

Db 277 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHLSLIFMAFFSEKKYLMGFT 325

RESULT 3

US-09-631-603-21

; Sequence 21, Application US/09631603

; Patent No. 6733990

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin R.

; APPLICANT: Lloyd, Clare

; APPLICANT: Weich, Nadine

; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the

; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof

; FILE REFERENCE: 5800-48A

; CURRENT FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 09/515,781

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 60/146,916

; PRIOR FILING DATE: 2000-08-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 21

; LENGTH: 593

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-631-603-21

Query Match 11.3%; Score 49; DB 4; Length 593;

Best Local Similarity 100.0%; Pred. No. 4.4e-36;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHLSLIFMAFFSEKKYLMGFT 169

Db 277 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHLSLIFMAFFSEKKYLMGFT 325

RESULT 4

US-09-826-509-563

; Sequence 563, Application US/09826509

; Patent No. 6806054

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 563

; LENGTH: 593

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-563

Query Match 11.3%; Score 49; DB 4; Length 593;

Best Local Similarity 100.0%; Pred. No. 4.4e-36;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFPLFLATNYWILVEGLYHLSLIFMAFFSEKKYLMGFT 169
Db 277 GYACRVAVTFPLFLATNYWILVEGLYHLSLIFMAFFSEKKYLMGFT 325

RESULT 5

US-08-811-519-31
; Sequence 31, Application US/08811519B
; Patent No. 6630345
; GENERAL INFORMATION:
; APPLICANT: Petrenko, Alexandre
; TITLE OF INVENTION: CALCIUM INDEPENDENT RECEPTOR OF ALPHA-LATROTOXIN,
; FILE REFERENCE: 1049-1-007
; CURRENT APPLICATION NUMBER: US/08/811,519B
; CURRENT FILING DATE: 1997-03-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-811-519-31

Query Match 11.0%; Score 48; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.4e-35;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 YACRVAVTFPLFLATNYWILVEGLYHLSLIFMAFFSEKKYLMGFT 169
Db 55 YACRVAVTFPLFLATNYWILVEGLYHLSLIFMAFFSEKKYLMGFT 102

RESULT 6

US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-18

Query Match 7.8%; Score 34; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 251
Db 368 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 401

RESULT 7

US-08-142-439A-6
; Sequence 6, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56703600 No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
US-08-142-439A-6

Query Match 7.8%; Score 34; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 251

Db 368 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 401

RESULT 8
US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; NUMBER OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
US-08-142-551B-125

Query Match 7.8%; Score 34; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 251
|||||

Db 368 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 401

RESULT 9
US-08-869-477-6
; Sequence 6, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1

; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747to No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-8201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
US-08-869-477-6

Query Match 7.8%; Score 34; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 251
|||||

Db 368 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 401

RESULT 10
US-08-468-249A-19
; Sequence 19, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-19

Query Match 7.8%; Score 34; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 NFILFINIIRVLATKLRNTAGRCDTROQYRKLL 251
Db 368 NFILFINIIRVLATKLRNTAGRCDTROQYRKLL 401

RESULT 11
US-08-468-011A-24
; Sequence 24, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
```

```
;
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-24

Query Match 7.1%; Score 31; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 QMHEYMLFNSFQGFVVAIIYFCNCGEVQAEI 314
Db 8 QMHEYMLFNSFQGFVVAIIYFCNCGEVQAEI 38

RESULT 12
US-09-236-468A-24
; Sequence 24, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Didelphis virginiana
; US-09-236-468A-24

Query Match 7.1%; Score 31; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 QMHEYMLFNSFQGFVVAIIYFCNCGEVQAEI 314
Db 8 QMHEYMLFNSFQGFVVAIIYFCNCGEVQAEI 38

RESULT 13
US-08-468-011A-14
; Sequence 14, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
```

```
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-14

Query Match 6.7%; Score 29; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 INIIRVLATKLRITNAGRCDTROQYRKLL 251
Db 1 INIIRVLATKLRITNAGRCDTROQYRKLL 29

RESULT 14
US-09-236-468A-14
; Sequence 14, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Didelphis virginiana
; US-09-236-468A-14

Query Match 6.7%; Score 29; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 INIIRVLATKLRITNAGRCDTROQYRKLL 251
Db 1 INIIRVLATKLRITNAGRCDTROQYRKLL 29

RESULT 15
US-09-449-632-2
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHr Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
```

```
; ORGANISM: zebrafish
US-09-449-632-2
```

```
Query Match 6.4%; Score 28; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 224 NIIRVLATKLRITNAGRCDTROQYRKLL 251
Db 334 NIIRVLATKLRITNAGRCDTROQYRKLL 361
```

```
Search completed: July 4, 2005, 06:31:15
Job time : 30 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 06:29:11 ; Search time 80 Seconds
(without alignments)
2097.762 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 435

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSRPPPLQEGWETVM 435

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1722376 seqs, 385795295 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1722376

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410	94.3	591	14	US-10-267-730-20
2	404	92.9	591	9	US-09-943-446-7
3	318	73.1	591	9	US-09-943-446-8
4	49	11.3	593	9	US-09-943-446-9
5	49	11.3	593	10	US-09-826-509-563
6	49	11.3	593	14	US-10-225-567A-229
7	49	11.3	593	14	US-10-267-730-21
8	49	11.3	593	16	US-10-723-860-1006
9	49	11.3	593	17	US-10-925-095-563
10	49	11.3	593	17	US-10-505-486-13
11	49	11.3	595	9	US-09-943-446-6
					Sequence 20, Appl
					Sequence 7, Appl
					Sequence 8, Appl
					Sequence 9, Appl
					Sequence 563, App
					Sequence 229, App
					Sequence 21, Appl
					Sequence 1006, App
					Sequence 563, App
					Sequence 13, Appl
					Sequence 6, Appl

12	43	9.9	964	14	US-10-017-161-710	Sequence 710, App
13	43	9.9	964	15	US-10-292-798-622	Sequence 622, App
14	34	7.8	515	14	US-10-267-730-18	Sequence 18, Appl
15	34	7.8	585	14	US-10-267-730-19	Sequence 19, Appl
16	31	7.1	59	9	US-09-996-569-24	Sequence 24, Appl
17	31	7.1	59	17	US-10-921-218-24	Sequence 24, Appl
18	29	6.7	52	9	US-09-996-569-14	Sequence 14, Appl
19	29	6.7	52	17	US-10-921-218-14	Sequence 14, Appl
20	28	6.4	536	14	US-10-372-095-2	Sequence 2, Appl
21	25	5.7	60	9	US-09-996-569-10	Sequence 10, Appl
22	25	5.7	60	17	US-10-921-218-10	Sequence 10, Appl
23	25	5.7	575	14	US-10-372-095-5	Sequence 5, Appl
24	24	5.5	25	14	US-10-267-730-13	Sequence 13, Appl
25	24	5.5	26	14	US-10-267-730-8	Sequence 8, Appl
26	19	4.4	19	14	US-10-225-567A-1231	Sequence 1231, App
27	19	4.4	19	14	US-10-267-730-7	Sequence 7, Appl
28	19	4.4	19	14	US-10-267-730-22	Sequence 22, Appl
29	18	4.1	19	14	US-10-267-730-6	Sequence 6, Appl
30	18	4.1	60	9	US-09-996-569-9	Sequence 9, Appl
31	18	4.1	60	17	US-10-921-218-9	Sequence 9, Appl
32	18	4.1	541	9	US-09-996-569-2	Sequence 2, Appl
33	18	4.1	541	17	US-10-921-218-2	Sequence 2, Appl
34	18	4.1	542	14	US-10-372-095-4	Sequence 4, Appl
35	18	4.1	546	14	US-10-014-162-109	Sequence 109, App
36	18	4.1	550	10	US-09-826-505-565	Sequence 565, App
37	18	4.1	550	14	US-10-225-567A-227	Sequence 227, App
38	18	4.1	550	15	US-10-295-027-526	Sequence 526, App
39	18	4.1	550	15	US-10-295-027-851	Sequence 851, App
40	18	4.1	550	16	US-10-723-860-2139	Sequence 2139, App
41	18	4.1	550	17	US-10-925-095-565	Sequence 565, App
42	18	4.1	561	15	US-10-295-027-524	Sequence 524, App
43	15	3.4	18	14	US-10-267-730-23	Sequence 23, Appl
44	15	3.4	60	9	US-09-996-569-19	Sequence 19, Appl
45	15	3.4	60	9	US-09-996-569-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-10-267-730-20
; Sequence 20, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-267-730-20

Query Match 94.3%; Score 410; DB 14; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRGLMITYGVGYSMSLASLTAVLILAYFRLHCTRYIHMHMFLSFMRLRAASIFVKD 85

Db 182 EVFDRGLMITYGVGYSMSLASLTAVLILAYFRLHCTRYIHMHMFLSFMRLRAASIFVKD 241

QY 86 AVLYSGFTLDEAERLTTELHIIAQVPPPPAAAAGVACRVATFFFLYFLATNYWILV 145

Db 242 AVLYSGFTLDEAERLTTEELHIIAQVPPPPAAAVGAGCRVAVTFFLYLATNYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRAVLANTGCWDLSSGHKKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRAVLANTGCWDLSSGHKKW 361
Qy 206 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
Db 362 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCDDTROQYRKLRLSTLVLPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVVAIYFCNCEVQAEIRKSWRWTLAL 325
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVVAIYFCNCEVQAEIRKSWRWTLAL 481
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNHGSQLPCHAKPGA 385
Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNHGSQLPCHAKPGA 541
Qy 386 PATETETLPVTMAVPKDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 435
Db 542 PATETETLPVTMAVPKDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 591

RESULT 2

US-09-943-446-7
; Sequence 7, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus No. US20020146777Alvegicus
US-09-943-446-7

Query Match 92.9%; Score 404; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRRLHCTRNHYHMHMFLSFMLRAASIFVKD 85
Db 182 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRRLHCTRNHYHMHMFLSFMLRAASIFVKD 241
Qy 86 AVLYSGFTLDEAERLTTEELHIIAQVPPPPAAAVGAGCRVAVTFFLYLATNYWILV 145
Db 242 AVLYSGFTLDEAERLTTEELHIIAQVPPPPAAAVGAGCRVAVTFFLYLATNYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRAVLANTGCWDLSSGHKKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRAVLANTGCWDLSSGHKKW 361
Qy 206 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
Db 362 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCDDTROQYRKLRLSTLVLPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVVAIYFCNCEVQAEIRKSWRWTLAL 325
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVVAIYFCNCEVQAEIRKSWRWTLAL 481
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNHGSQLPCHAKPGA 385

Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNHGSQLPCHAKPGA 541
Qy 386 PATETETLPVTMAVPKDDGFLNGSCGLDEEASGSARPPPLLOE 429
Db 542 PATETETLPVTMAVPKDDGFLNGSCGLDEEASGSARPPPLLOE 585

RESULT 3

US-09-943-446-8
; Sequence 8, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-943-446-8

Query Match 73.1%; Score 318; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.4e-292;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRRLHCTRNHYHMHMFLSFMLRAASIFVKD 85
Db 182 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRRLHCTRNHYHMHMFLSFMLRAASIFVKD 241
Qy 86 AVLYSGFTLDEAERLTTEELHIIAQVPPPPAAAVGAGCRVAVTFFLYLATNYWILV 145
Db 242 AVLYSGFTLDEAERLTTEELHIIAQVPPPPAAAVGAGCRVAVTFFLYLATNYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRAVLANTGCWDLSSGHKKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRAVLANTGCWDLSSGHKKW 361
Qy 206 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
Db 362 IIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCDDTROQYRKLRLSTLVLPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVVAIYFCNCEVQAEIRKSWRWTLAL 325
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVVAIYFCNCEVQAEIRKSWRWTLAL 481
Qy 326 DFKRKARSGSSSYSGPM 343
Db 482 DFKRKARSGSSSYSGPM 499

RESULT 4

US-09-943-446-9
; Sequence 9, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR


```
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-943-446-9

Query Match      11.3%; Score 49; DB 9; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
Db 277 GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 5
US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match      11.3%; Score 49; DB 10; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
Db 277 GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 6
US-10-225-567A-229
; Sequence 229, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
```

```
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-229

Query Match      11.3%; Score 49; DB 14; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
Db 277 GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 7
US-10-267-730-21
; Sequence 21, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match      11.3%; Score 49; DB 14; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
Db 277 GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 8
US-10-723-860-1006
; Sequence 1006, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882, 0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1006
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1006

Query Match      11.3%; Score 49; DB 16; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
```

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 277 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 325

RESULT 9
US-10-925-095-563
; Sequence 563, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-563

Query Match 11.3%; Score 49; DB 17; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 277 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 325

RESULT 10
US-10-505-486-13
; Sequence 13, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 13
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-13

Query Match 11.3%; Score 49; DB 17; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 277 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 325

RESULT 11
US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Query Match 11.3%; Score 49; DB 9; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 276 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 324

RESULT 12
US-10-017-161-710
; Sequence 710, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-710

Query Match 9.9%; Score 43; DB 14; Length 964;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 VAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 557 VAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 599

RESULT 13
US-10-292-798-622
; Sequence 622, Application US/10292798
; Publication No. US2003023583A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO

; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-622

Query Match 9.9%; Score 43; DB 15; Length 964;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 VAVTFEFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFT 169
Db 557 VAVTFEFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFT 599

RESULT 14
US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match 7.8%; Score 34; DB 14; Length 515;
Best Local Similarity 100.0%; Pred. No. 4.2e-23;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 251
Db 368 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 401

RESULT 15
US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina

; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match 7.8%; Score 34; DB 14; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.7e-23;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 251
Db 368 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 401

Search completed: July 4, 2005, 06:36:45
Job time : 81 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 06:13:35 ; Search time 26 Seconds
(without alignments)
1609.780 Million cell updates/sec

Title: US-09-869-565-2
Perfect score: 435
Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGARPPPLQGWETVM 435

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	92.9	591	2 154195	parathyroid hormon
2	318	73.1	591	2 544203	parathyroid hormon
3	282	64.8	589	2 159297	parathyroid hormon
4	49	11.3	593	2 A49191	parathyroid hormon
5	34	7.8	585	2 A39286	parathyroid hormon
6	18	4.1	550	2 A57519	parathyroid hormon
7	14	3.2	440	2 JC2532	secretin receptor
8	14	3.2	449	2 S16319	secretin receptor
9	14	3.2	482	2 A39285	calcitonin recepto
10	14	3.2	498	2 I47130	calcitonin recepto
11	13	3.0	455	2 153273	gastric inhibitory
12	13	3.0	462	2 JC2462	gastric inhibitory
13	12	2.8	466	2 G02234	gastric inhibitory
14	12	2.8	466	2 S66676	glucose-dependent
15	12	2.8	491	2 I37411	glucose-dependent
16	11	2.5	459	2 JH0594	vasoactive intesti
17	11	2.5	460	2 JC2194	vasoactive intesti
18	11	2.5	495	2 JC2195	vasoactive intesti
19	9	2.1	437	2 JU0185	PACAP/VIP receptor
20	9	2.1	437	2 S39059	vasoactive intesti
21	9	2.1	438	2 G02822	vasoactive intesti
22	9	2.1	463	2 S71624	glucagon-like pept
23	9	2.1	463	2 I84494	glucagon-like pept
24	9	2.1	463	2 A46172	glucagon-like pept
25	9	2.1	485	2 JC4363	glucagon receptor
26	9	2.1	485	2 J01957	glucagon receptor
27	9	2.1	865	2 S77440	hypothetical prote
28	8	1.8	304	2 T27680	hypothetical prote
29	8	1.8	306	2 T09067	extensin-like prot

ALIGNMENTS

RESULT 1

I54195

parathyroid hormone/parathyroid hormone related-peptide receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C;Accession: I54195; A42698

R;Pausova, Z.; Bourdon, J.; Clayton, D.; Mattel, M.G.; Seldin, M.F.; Janicic, N.; Rivier

Genomics 20, 20-26, 1994

A;Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (and rat genomes.

A;Reference number: I54195; MUID:94292182; PMID:8020952

A;Accession: I54195

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-591 <RES>

A;Cross-references: UNIPROT:P25961; GB:L19475; NID:9467316; PIDN:AAA68098.1; PID:9467317

R;Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure

Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992

A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid

n of both cAMP and inositol trisphosphates and increases intracellular free calcium.

A;Reference number: A42698; MUID:92212903; PMID:1313566

A;Accession: A42698

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-585,'G',587-591 <ABO>

A;Experimental source: ROS 17/2.8 osteosarcoma cells

A;Note: sequence extracted from NCBI backbone (NCBIP:92187)

C;Superfamily: glucagon receptor

Query Match 92.9%; Score 404; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	26	EVFDRGLMIVTVGYSMASLTVAVLILAYFRRLHCTRNIIHMHMFLSFLMLRAASIFVKD	85
Db	182	EVFDRGLMIVTVGYSMASLTVAVLILAYFRRLHCTRNIIHMHMFLSFLMLRAASIFVKD	241
Qy	86	AVLYSGFTLDEARLTFEELHIIAQVPPPPAAAVGACRVAVTFPLFLATNYWILV	145
Db	242	AVLYSGFTLDEARLTFEELHIIAQVPPPPAAAVGACRVAVTFPLFLATNYWILV	301
Qy	146	EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRATLANTGWDLSGGHKW	205
Db	302	EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRATLANTGWDLSGGHKW	361
Qy	206	IIQVPIIASVVLNFIPIINIRVLATKLRETNAGRCOTRQOYRKLLASTLVLPFGVHY	265
Db	362	IIQVPIIASVVLNFIPIINIRVLATKLRETNAGRCOTRQOYRKLLASTLVLPFGVHY	421
Qy	266	TVFMALPYTEVSGTLWQIQMHYEMFLNSFGQFFVAILIYFCNGEVSQAEIKSRWTLAL	325
Db	422	TVFMALPYTEVSGTLWQIQMHYEMFLNSFGQFFVAILIYFCNGEVSQAEIKSRWTLAL	481

protein M01D7.2 [i
hypothetical prote
transcription fact
glucose-1-phosphat
glucose-1-phosphat
pituitary adenylat
pituitary adenylat
gene gfi-2 protein
hypothetical prote
glucagon receptor
pituitary adenylat
pituitary adenylat
pituitary adenylat
pituitary adenylat
EIA-associated cyc

QY 326 DEKKKARSGSSSYSGPMVSHTSVTNVPAGLSLPLSPRLPATTTNGHSQLPCHAKPGA 385
|||||
Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVPAGLSLPLSPRLPATTTNGHSQLPCHAKPGA 541
|||||
QY 386 PATETETLPVTMAVPKDDGFLNGSCSLDEEASGSARPPPLLOE 429
|||||
Db 542 PATETETLPVTMAVPKDDGFLNGSCSLDEEASGSARPPPLLOE 585
|||||

RESULT 2
S44203
parathyroid hormone-related peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S44203
R;Karperien, M.; van Diik, T.B.; Hoeljmackers, T.; Cremers, F.; Abou-Samra, A.B.; Boonst
submitted to the EMBL Data Library, April 1994
A;Description: Expression pattern of parathyroid hormone/parathyroid hormone related pe
A;Reference number: S44203
A;Accession: S44203
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-591 <R>
A;Cross-references: UNIPROT:P41593; EMBL:X78936; NID:9474828; PIDN:CAA55536.1; PID:94748
C;Superfamily: glucagon receptor

Query Match 73.1%; Score 318; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.2e-309;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLGMIYTVGYSMSLASITVAVLLIAYFRRLHCTCRNYIHMHMFLSFMRLRAASIFVKD 85
|||||
Db 182 EVFDRLGMIYTVGYSMSLASITVAVLLIAYFRRLHCTCRNYIHMHMFLSFMRLRAASIFVKD 241
|||||
QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAVGAGCRVAVTFPLYFLATNYWILV 145
|||||
Db 242 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAVGAGCRVAVTFPLYFLATNYWILV 301
|||||
QY 146 EGYLHSLIFMAFFSEKKYIWMGFTIFGWLPAVFAVAVWVGVTRATLANTGCWDLSSGHKKW 205
|||||
Db 302 EGYLHSLIFMAFFSEKKYIWMGFTIFGWLPAVFAVAVWVGVTRATLANTGCWDLSSGHKKW 361
|||||
QY 206 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLVPLFGVHY 265
|||||
Db 362 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLVPLFGVHY 421
|||||
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVVAIYFCFN 307
|||||
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVVAIYFCFN 463
|||||

RESULT 3
S44203
parathyroid hormone-related-peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59297
R;McCuig, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A;Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyro
A;Reference number: I59297; MUID:94255468; PMID:8197183
A;Accession: I59297
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-589 <R>
A;Cross-references: UNIPROT:P41593; GB:L34611; NID:G530149; PIDN:AAA40011.1; PID:G530151
C;Genetics:
A;Gene: PTHR

A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 451/3
C;Superfamily: glucagon receptor

Query Match 64.8%; Score 282; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 6.2e-273;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLGMIYTVGYSMSLASITVAVLLIAYFRRLHCTCRNYIHMHMFLSFMRLRAASIFVKD 85
|||||
Db 182 EVFDRLGMIYTVGYSMSLASITVAVLLIAYFRRLHCTCRNYIHMHMFLSFMRLRAASIFVKD 241
|||||
QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAVGAGCRVAVTFPLYFLATNYWILV 145
|||||
Db 242 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAVGAGCRVAVTFPLYFLATNYWILV 301
|||||
QY 146 EGYLHSLIFMAFFSEKKYIWMGFTIFGWLPAVFAVAVWVGVTRATLANTGCWDLSSGHKKW 205
|||||
Db 302 EGYLHSLIFMAFFSEKKYIWMGFTIFGWLPAVFAVAVWVGVTRATLANTGCWDLSSGHKKW 361
|||||
QY 206 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLVPLFGVHY 265
|||||
Db 362 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLVPLFGVHY 421
|||||
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVVAIYFCFN 307
|||||
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVVAIYFCFN 463
|||||

RESULT 4
A49191
parathyroid hormone/PTH-related peptide receptor - human
N;Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: I38139; A49191; I38113; G01562; S29610
R;Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.;
Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995
A;Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons
A;Reference number: I38139; MUID:95263723; PMID:7745008
A;Accession: I38139
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-593 <R>
A;Cross-references: UNIPROT:Q03431; EMBL:U22409; NID:9897594; PIDN:AAB60657.1; PID:989759;
R;Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.
Endocrinology 132, 2157-2165, 1993
A;Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa
A;Reference number: A49191; MUID:93238641; PMID:8386612
A;Accession: A49191
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-593 <SCH>
A;Cross-references: GB:I04308; NID:gi90721; PIDN:AAA36525.1; PID:gi90722
A;Note: sequence extracted from NCBI backbone (NCBIN:I30233, NCBIP:I30234)
R;Schneider, H.; Feven, J.H.; Seuwen, K.; Movva, N.R.
Eur. J. Pharmacol. 246, 149-155, 1993
A;Title: Cloning and functional expression of a human parathyroid hormone receptor.
A;Reference number: I38113; MUID:93387403; PMID:8397094
A;Accession: I38113
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-593 <RE2>
A;Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813
R;Levine, M.
submitted to the EMBL Data Library, November 1994
A;Reference number: G07787
A;Accession: G01562
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-593 <LEV>
A;Cross-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130
C;Genetics:

JC2532
secretin receptor - human
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: JC2532
R:Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A:Title: Molecular cloning and functional expression of a human pancreatic secretin receptor
A:Reference number: JC2532; MUID:95169147; PMID:7864894
A:Accession: JC2532
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <JIA>
A:Cross-references: UNIPROT:P47872; EMBL:U20178; NID:g662795; PIDN:AAC50106.1; PID:g662795
A:Experimental source: pancreas
C:Genetics:
A:Gene: GDB: SCTP
A:Cross-references: GDB:270546; OMIM:182098
A:Map position: 2q14.1-2q14.1
C:Superfamily: glucagon receptor

Query Match 3.2%; Score 14; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 56 FRLHCTRNYYIHMH 69
 |||||
Db 167 FRLHCTRNYYIHMH 180

RESULT 8
S16319
secretin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S16319
R:Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO J. 10, 1635-1641, 1991
A:Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A:Reference number: S16319; MUID:91266890; PMID:1646711
A:Accession: S16319
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-449 <ISH>
A:Cross-references: UNIPROT:P23811; EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57228
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.2%; Score 14; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 56 FRLHCTRNYYIHMH 69
 |||||
Db 167 FRLHCTRNYYIHMH 180

RESULT 9
A39285
calcitonin receptor-la precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C:Accession: A39285; I47129
R:Lin, H.Y.; Harris, T.L.; Flannery, M.S.; Aruffo, A.; Kaji, E.H.; Gorn, A.; Kolakowski
Science 254, 1022-1024, 1991
A:Title: Expression cloning of an adenylate cyclase-coupled calcitonin receptor.
A:Reference number: A39285; MUID:92054591; PMID:1658940
A:Accession: A39285
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-482 <LIN>
A:Cross-references: UNIPROT:P25117; GB:M74420; NID:gl64430; PIDN:AAA31023.1; PID:gl64431
R:Zolnierowicz, S.; Cron, P.; Solinas-Toldo, S.; Fries, R.; Lin, H.Y.; Hemmings, B.A.

J. Biol. Chem. 269, 19530-19538, 1994
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 147129
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-482 <ZOL>
A;Cross-references: EMBL:Z31356; NID:g531126; PIDN:CAA83232.1; PID:g531127
C;Genetics:
A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 217/3; 269/1; 289/2; 311/3; 384/3; 398/3
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.2%; Score 14; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 FQGFVAILIYCFN 307
DB 383 FQGFVAILIYCFN 396
|||||

RESULT 10
147130
calcitonin receptor-1b - pig
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 147130
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-498 <ZOL>
A;Cross-references: UNIPROT:P25117; EMBL:Z31356; NID:g531126; PIDN:CAA83233.1; PID:g531127
C;Genetics:
A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 233/3; 285/1; 305/2; 327/3; 400/3; 414/3
C;Superfamily: glucagon receptor

Query Match 3.2%; Score 14; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 FQGFVAILIYCFN 307
DB 399 FQGFVAILIYCFN 412
|||||

RESULT 11
153273
gastric inhibitory polypeptide receptor - rat
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 153273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-455 <RES>
A;Cross-references: UNIPROT:P43219; GB:L19660; NID:g431448; PIDN:AAC37637.1; PID:g431449
C;Superfamily: glucagon receptor

Query Match 3.0%; Score 13; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 FRRLHCTRNVIH 68
|||||

Db 159 FRRLHCTRNVIH 171
|||||

RESULT 12
JC2462
gastric inhibitory polypeptide receptor - hamster
N;Alternate names: GIP receptor
C;Species: Cricetineae gen. sp. (hamster)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
A;Accession: JC2462
R;Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A;Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic islets
A;Reference number: JC2462; MUID:95110292; PMID:7811236
A;Accession: JC2462
A;Molecule type: mRNA
A;Residues: 1-462 <YAS>
A;Cross-references: DDBJ:D38103; NID:g644880; PIDN:BAA07284.1; PID:g765087
C;Superfamily: glucagon receptor
C;Keywords: receptor; transmembrane protein
F;136-157/Domain: transmembrane #status predicted <TM1>
F;167-186/Domain: transmembrane #status predicted <TM2>
F;215-238/Domain: transmembrane #status predicted <TM3>
F;252-274/Domain: transmembrane #status predicted <TM4>
F;292-315/Domain: transmembrane #status predicted <TM5>
F;339-357/Domain: transmembrane #status predicted <TM6>
F;383-394/Domain: transmembrane #status predicted <TM7>

Query Match 3.0%; Score 13; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 FRRLHCTRNVIH 68
DB 159 FRRLHCTRNVIH 171
|||||

RESULT 13
G02234
gastric inhibitory polypeptide receptor - human
N;Alternate names: GIP receptor
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
A;Accession: G02234
R;Bonner, T.I.; Usdin, T.B.
submitted to the EMBL Data Library, October 1995
A;Reference number: G09336
A;Accession: G02234
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-466 <BON>
A;Cross-references: UNIPROT:P48546; EMBL:U39231; NID:g1066050; PIDN:AAA84418.1; PID:g1066050
C;Genetics:
A;Gene: GDB:GIPR
A;Cross-references: GDB:335023
A;Map position: 19q13.3-19q13.3
C;Superfamily: glucagon receptor

Query Match 2.8%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 FRRLHCTRNVIH 67
DB 162 FRRLHCTRNVIH 173
|||||

RESULT 14
S66676
glucose-dependent insulintropic protein receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66676

R;Volz, A.; Goeke, R.; Lankat-Buttgereit, B.; Fehmann, H.C.; Bode, H.P.; Goeke, B.
FEBS Lett. 373, 23-29, 1995
A;Title: Molecular cloning, functional expression, and signal transduction of the GIP-re
A;Reference number: S66676; MUID:96013879; PMID:7589426
A;Accession: S66676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <VOL>
A;Cross-references: UNIPROT:P48546; GB:S79852
A;Note: the authors translated the codon GCC for residue 427 as Leu
C;Superfamily: glucagon receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-466/Product: glucose-dependent insulinotropic protein receptor #status predicted <M

Query Match 2.8%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 FRLHCTRNYYH 67
| | | | | | | | | |
Db 162 FRLHCTRNYYH 173

RESULT 15

I37411
glucose-dependent insulinotropic polypeptide receptor - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999
C;Accession: I37411
R;Gremlich, S.; Porret, A.; Hani, E.H.; Cherif, D.; Vionnet, N.; Froguel, P.; Thorens, B.
Diabetes 44, 1202-1208, 1995
A;Title: Cloning, functional expression, and chromosomal localization of the human pancr
A;Reference number: I37411; MUID:96007224; PMID:7556958
A;Accession: I37411
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-491 <RES>
A;Cross-references: EMBL:X81832; NID:gl030050; PIDN:CAA57426.1; PID:gl030051
C;Superfamily: glucagon receptor

Query Match 2.8%; Score 12; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 FRLHCTRNYYH 67
| | | | | | | | | |
Db 161 FRLHCTRNYYH 172

Search completed: July 4, 2005, 06:29:04
Job time : 28 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2005, 06:17:00 ; Search time 91 Seconds
(without alignments)
2447.851 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 435

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLQEGWETVM 435

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	92.9	591	1 PTHR RAT	P25961 rattus norv
2	341	78.4	591	2 Q80WU8	Q80WU8 mus musculu
3	338	77.7	591	2 Q91WV4	Q91WV4 mus musculu
4	318	73.1	591	1 PTHR MOUSE	P41593 mus musculu
5	141	32.4	147	2 Q76N28	Q76N28 rattus norv
6	49	11.3	593	1 PTHR HUMAN	Q03431 homo sapien
7	49	11.3	595	2 Q9TU31	Q9TU31 canis fami
8	46	10.6	585	1 PTHR PIG	P50133 sus scrofa
9	43	9.9	589	2 Q9GMD1	Q9GMD1 oryctolagus
10	43	9.9	964	2 Q8NHB4	Q8NHB4 homo sapien
11	40	9.2	589	2 Q7YR13	Q7YR13 cervus elap
12	34	7.8	585	1 PTHR DIDMA	P25107 didelphis m
13	28	6.4	536	2 Q9PVD3	Q9PVD3 brachydanio
14	27	6.2	94	2 Q9PRG1	Q9PRG1 ictalurus p
15	26	6.0	126	2 Q57671	Q57671 meleagris g
16	25	5.7	575	2 Q9PBW7	Q9PBW7 brachydanio
17	18	4.1	542	2 Q9PVD2	Q9PVD2 brachydanio
18	18	4.1	546	1 PTHR MOUSE	Q91V95 mus musculu
19	18	4.1	546	1 PTHR RAT	P70555 rattus norv
20	18	4.1	550	1 PTHR HUMAN	P49190 homo sapien
21	15	3.4	24	2 Q71UK6	Q71UK6 homo sapien
22	14	3.2	440	1 SCRC HUMAN	Q81872 homo sapien
23	14	3.2	440	2 SCRC HUMAN	Q81872 homo sapien
24	14	3.2	445	1 SCRC RABIT	Q46502 oryctolagus
25	14	3.2	449	1 SCRC RAT	P23811 rattus norv
26	14	3.2	498	1 CALR PIG	P25117 sus scrofa
27	13	3.0	162	2 Q80UB4	Q80UB4 mus musculu
28	13	3.0	169	2 Q9R1D4	Q9R1D4 mus musculu
29	13	3.0	455	1 GIPR RAT	P43219 rattus norv
30	13	3.0	462	1 GIPR MESAU	P43218 mesocricetu
31	12	2.8	425	2 Q802T7	Q802T7 fugu rubrip

32	12	2.8	440	2	Q64FL4	Q64FL4 oncorhynch
33	12	2.8	466	1	GIPR HUMAN	P48546 homo sapien
34	11	2.5	418	2	Q91BG2	Q91BG2 gallus gall
35	11	2.5	419	2	Q8AXV3	Q8AXV3 fugu rubrip
36	11	2.5	435	2	Q64FL3	Q64FL3 oncorhynch
37	11	2.5	444	2	Q9VHC6	Q9VHC6 rana ridibu
38	11	2.5	447	1	VIPR_CARAU	Q90308 carassius a
39	11	2.5	457	1	VIPR_HUMAN	P32241 homo sapien
40	11	2.5	457	1	VIPR_MELGA	Q91085 meleagris g
41	11	2.5	457	2	Q6P2M6	Q6P2M6 homo sapien
42	11	2.5	458	1	VIPR_PIG	Q28992 sus scrofa
43	11	2.5	459	1	VIPR_MOUSE	P97751 mus musculu
44	11	2.5	459	1	VIPR_RAT	P30093 rattus norv
45	10	2.3	48	2	Q9JUI4	Q9JUI4 mus musculu

ALIGNMENTS

RESULT 1

ID	PTHR RAT	STANDARD;	PRT;	591 AA.
AC	P25961;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Parathyroid hormone/parathyroid hormone-related peptide receptor			
DE	precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).			
GN	Name=Pthrl; Synonyms=Pthr;			
OS	Rattus norvegicus (Rat).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone;			
RX	MEDLINE=92212903; PubMed=1313566;			
RA	Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,			
RA	Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,			
RA	Kronenberg H.M., Segre G.V.;			
RT	"Expression cloning of a common receptor for parathyroid hormone and			
RT	parathyroid hormone-related peptide from rat osteoblast-like cells: a			
RT	single receptor stimulates intracellular accumulation of both cAMP and			
RT	inositol triphosphates and increases intracellular free calcium.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94292182; PubMed=8020952;			
RA	Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F.,			
RA	Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;			
RT	"Cloning of a parathyroid hormone/parathyroid hormone-related peptide			
RT	receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line:			
RT	chromosomal assignment of the gene in the human, mouse, and rat			
RT	genomes.";			
RL	Genomics 20:20-26(1994).			
CC	-I- FUNCTION: This is a receptor for parathyroid hormone and for			
CC	parathyroid hormone-related peptide. The activity of this receptor			
CC	is mediated by g proteins which activate adenylyl cyclase and also			
CC	a phosphatidylinositol-calcium second messenger system.			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M77184; AAA1811.1; -;			
DR	EMBL; L19475; AAA68098.1; -;			
DR	PIR; I54195; I54195.			

DR	HSSP; Q03431; 1BL1.	DR	Q80WU8	PRELIMINARY;	PRT;	591 AA.
DR	RCD; 3442; Pthr1.	DR	Q80WU8			
DR	InterPro; IPR000832; GPCR_secretin.	DR	Q80WU8			
DR	InterPro; IPR001879; hormn_receptor.	DR	Q80WU8			
DR	Pfam; PF00002; 7tm_2; 1.	DR	Q80WU8			
DR	Pfam; PF02793; HRM; 1.	DR	Q80WU8			
DR	PRINTS; PR00249; GPCRSECRETIN.	DR	Q80WU8			
DR	SMART; SM00008; Hormr; 1.	DR	Q80WU8			
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.	DR	Q80WU8			
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.	DR	Q80WU8			
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.	DR	Q80WU8			
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.	DR	Q80WU8			
KW	G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.	DR	Q80WU8			
FT	SIGNAL 1 26	DR	Q80WU8			
FT	CHAIN 27 591	DR	Q80WU8			
FT	DOMAIN 27 188	DR	Q80WU8			
FT	TRANSMEM 189 212	DR	Q80WU8			
FT	DOMAIN 213 219	DR	Q80WU8			
FT	TRANSMEM 220 239	DR	Q80WU8			
FT	DOMAIN 240 282	DR	Q80WU8			
FT	TRANSMEM 283 306	DR	Q80WU8			
FT	DOMAIN 307 320	DR	Q80WU8			
FT	TRANSMEM 321 342	DR	Q80WU8			
FT	DOMAIN 343 361	DR	Q80WU8			
FT	TRANSMEM 362 382	DR	Q80WU8			
FT	DOMAIN 383 409	DR	Q80WU8			
FT	TRANSMEM 410 428	DR	Q80WU8			
FT	DOMAIN 429 440	DR	Q80WU8			
FT	TRANSMEM 441 463	DR	Q80WU8			
FT	DOMAIN 464 591	DR	Q80WU8			
FT	DISULFID 48 117	DR	Q80WU8			
FT	DISULFID 108 148	DR	Q80WU8			
FT	DISULFID 131 170	DR	Q80WU8			
FT	CARBOHYD 151 151	DR	Q80WU8			
FT	CARBOHYD 161 161	DR	Q80WU8			
FT	CARBOHYD 166 166	DR	Q80WU8			
FT	CARBOHYD 176 176	DR	Q80WU8			
FT	CARBOHYD 176 176	DR	Q80WU8			
SQ	SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;	DR	Q80WU8			
Query Match 92.9%; Score 404; DB 1; Length 591;		DR	Q80WU8			
Best Local Similarity 100.0%; Pred. No. 0;		DR	Q80WU8			
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		DR	Q80WU8			
Qy	26 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRLHCTRNIIHMHMFLSFMFLRAASIFVKD 85	DR	Q80WU8			
Db	182 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRLHCTRNIIHMHMFLSFMFLRAASIFVKD 241	DR	Q80WU8			
Qy	86 AVLYSGFTLDEARLTTEELHIIAQVPPPPAAAVGACRVAVTFLYFLATNYWILV 145	DR	Q80WU8			
Db	242 AVLYSGFTLDEARLTTEELHIIAQVPPPPAAAVGACRVAVTFLYFLATNYWILV 301	DR	Q80WU8			
Qy	146 EGLYLSLIFMAFFSEKKYLGWFTIFGWLPAVFAVWVGVRATLANTGCWDLSSGHKKW 205	DR	Q80WU8			
Db	302 EGLYLSLIFMAFFSEKKYLGWFTIFGWLPAVFAVWVGVRATLANTGCWDLSSGHKKW 361	DR	Q80WU8			
Qy	206 IIQVPILASVNLFIPIRVLATKLRTNAGRCDTROQYKLLRSTLVLPFGVHY 265	DR	Q80WU8			
Db	362 IIQVPILASVNLFIPIRVLATKLRTNAGRCDTROQYKLLRSTLVLPFGVHY 421	DR	Q80WU8			
Qy	266 TVFMALPYTEVSGTLWQIQMHEMLFNSFGFFVAILYFCNGEVOAEIRKSWRWTAL 325	DR	Q80WU8			
Db	422 TVFMALPYTEVSGTLWQIQMHEMLFNSFGFFVAILYFCNGEVOAEIRKSWRWTAL 481	DR	Q80WU8			
Qy	326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPGA 385	DR	Q80WU8			
Db	482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPGA 541	DR	Q80WU8			
Qy	386 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLQOE 429	DR	Q80WU8			
Db	542 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLQOE 585	DR	Q80WU8			
Query Match 78.4%; Score 341; DB 2; Length 591;		DR	Q80WU8			
Best Local Similarity 100.0%; Pred. No. 0;		DR	Q80WU8			
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		DR	Q80WU8			
Qy	26 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRLHCTRNIIHMHMFLSFMFLRAASIFVKD 85	DR	Q80WU8			
Db	182 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRLHCTRNIIHMHMFLSFMFLRAASIFVKD 241	DR	Q80WU8			
Qy	86 AVLYSGFTLDEARLTTEELHIIAQVPPPPAAAVGACRVAVTFLYFLATNYWILV 145	DR	Q80WU8			

```

Db 242 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 301
QY 146 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVRAVTLANTGCDLSSGHKKW 205
Db 302 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVRAVTLANTGCDLSSGHKKW 361
QY 206 IIQVPILASVNLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVHY 265
Db 362 IIQVPILASVNLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVHY 421
QY 266 TVFMALPYTEVSGTLQIQWHYEMLFNSFGQFFVAILIYCFNCEVQAEIRKSRMTLAL 325
Db 422 TVFMALPYTEVSGTLQIQWHYEMLFNSFGQFFVAILIYCFNCEVQAEIRKSRMTLAL 481
QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRL 366
Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRL 522

RESULT 3
Q91WV4 PRELIMINARY; PRT; 591 AA.
AC Q91WV4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor 1.
GN Name=Pthr1;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PVB/N, TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Caspieten M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faneay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N, TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013446; AAH13446.1; -.
DR HSSP; Q03431; 1BL1.
DR MGD; MGI:17801; Pthr1.
DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
DR GO; GO:0030282; P:bone mineralization; IMP.
DR GO; GO:0001501; P:skeletal development; IMP.
DR Pfam; PF00002; 7tm2; 1.
DR Pfam; PF02793; HRM1; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; PR00393; PTHRHMOMER.
DR SMART; SMO0008; HORMR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

```

```

DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 591 AA; 66361 MW; 6E29CF63E5BAFED CRC64;

Query Match 77.7%; Score 338; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRGLMITYGVSYMSLASLTAVLILAYFRLHCHTRNYIHHMFLSFMRLAASIFVKD 85
Db 182 EVFDRGLMITYGVSYMSLASLTAVLILAYFRLHCHTRNYIHHMFLSFMRLAASIFVKD 241
QY 86 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 145
Db 242 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 301
QY 146 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVRAVTLANTGCDLSSGHKKW 205
Db 302 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVRAVTLANTGCDLSSGHKKW 361
QY 206 IIQVPILASVNLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVHY 265
Db 362 IIQVPILASVNLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVHY 421
QY 266 TVFMALPYTEVSGTLQIQWHYEMLFNSFGQFFVAILIYCFNCEVQAEIRKSRMTLAL 325
Db 422 TVFMALPYTEVSGTLQIQWHYEMLFNSFGQFFVAILIYCFNCEVQAEIRKSRMTLAL 481
QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLS 363
Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLS 519

RESULT 4
PTRR_MOUSE STANDARD; PRT; 591 AA.
AC P41593; Q62119;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
GN Name=Pthr1; Synonyms=Pthr;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEHA;
RX MEDLINE=95034305; PubMed=7524627; DOI=10.1016/0925-4773(94)90093-0;
RA Karperien M., van Dijk T.B., Hosijsmakers T., Cremers F.,
RA Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
RT "Expression pattern of parathyroid hormone/parathyroid hormone related
RT peptide receptor mRNA in mouse postimplantation embryos indicates
RT involvement in multiple developmental processes.";
RL Mech. Dev. 47:29-42(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94255468; PubMed=8197183;
RA McCuaig K.A., Clarke J.C., White J.H.;
RT "Molecular cloning of the gene encoding the mouse parathyroid
RT hormone/parathyroid hormone-related peptide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
CC -1- FUNCTION: This is a receptor for parathyroid hormone and for
CC parathyroid hormone-related peptide. The activity of this receptor
CC is mediated by g proteins which activate adenylyl cyclase and also
CC a phosphatidylinositol-calcium second messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X78936; CAAS5536.1; -.
DR EMBL; L34611; AAA40011.1; -.
DR EMBL; L34608; AAA40011.1; JOINED.
DR EMBL; L34607; AAA40011.1; JOINED.
DR EMBL; L34609; AAA40011.1; JOINED.
DR EMBL; L34610; AAA40011.1; JOINED.
DR PIR; I59297; -.
DR PIR; S44203; S44203.
DR HSSP; Q03431; 1BL1.
DR MGD; MGI:97801; Pthr1.
DR GO; GO:0030282; P.bone mineralization; IMP.
DR GO; GO:0001501; P.skeletal development; IMP.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HormR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECIP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECIP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECIP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECIP_F2_4; 1.
DR G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
KW SIGNAL
FT CHAIN 1 26
FT DOMAIN 27 591
FT Parathyroid hormone/parathyroid hormone-
FT related peptide receptor.
FT Extracellular (Potential).
FT 1 (Potential).
FT 2 (Potential).
FT 3 (Potential).
FT 4 (Potential).
FT 5 (Potential).
FT 6 (Potential).
FT 7 (Potential).
FT 8 (Potential).
FT 9 (Potential).
FT 10 (Potential).
FT 11 (Potential).
FT 12 (Potential).
FT 13 (Potential).
FT 14 (Potential).
FT 15 (Potential).
FT 16 (Potential).
FT 17 (Potential).
FT 18 (Potential).
FT 19 (Potential).
FT 20 (Potential).
FT 21 (Potential).
FT 22 (Potential).
FT 23 (Potential).
FT 24 (Potential).
FT 25 (Potential).
FT 26 (Potential).
FT 27 (Potential).
FT 28 (Potential).
FT 29 (Potential).
FT 30 (Potential).
FT 31 (Potential).
FT 32 (Potential).
FT 33 (Potential).
FT 34 (Potential).
FT 35 (Potential).
FT 36 (Potential).
FT 37 (Potential).
FT 38 (Potential).
FT 39 (Potential).
FT 40 (Potential).
FT 41 (Potential).
FT 42 (Potential).
FT 43 (Potential).
FT 44 (Potential).
FT 45 (Potential).
FT 46 (Potential).
FT 47 (Potential).
FT 48 (Potential).
FT 49 (Potential).
FT 50 (Potential).
FT 51 (Potential).
FT 52 (Potential).
FT 53 (Potential).
FT 54 (Potential).
FT 55 (Potential).
FT 56 (Potential).
FT 57 (Potential).
FT 58 (Potential).
FT 59 (Potential).
FT 60 (Potential).
FT 61 (Potential).
FT 62 (Potential).
FT 63 (Potential).
FT 64 (Potential).
FT 65 (Potential).
FT 66 (Potential).
FT 67 (Potential).
FT 68 (Potential).
FT 69 (Potential).
FT 70 (Potential).
FT 71 (Potential).
FT 72 (Potential).
FT 73 (Potential).
FT 74 (Potential).
FT 75 (Potential).
FT 76 (Potential).
FT 77 (Potential).
FT 78 (Potential).
FT 79 (Potential).
FT 80 (Potential).
FT 81 (Potential).
FT 82 (Potential).
FT 83 (Potential).
FT 84 (Potential).
FT 85 (Potential).
FT 86 (Potential).
FT 87 (Potential).
FT 88 (Potential).
FT 89 (Potential).
FT 90 (Potential).
FT 91 (Potential).
FT 92 (Potential).
FT 93 (Potential).
FT 94 (Potential).
FT 95 (Potential).
FT 96 (Potential).
FT 97 (Potential).
FT 98 (Potential).
FT 99 (Potential).
FT 100 (Potential).
FT 101 (Potential).
FT 102 (Potential).
FT 103 (Potential).
FT 104 (Potential).
FT 105 (Potential).
FT 106 (Potential).
FT 107 (Potential).
FT 108 (Potential).
FT 109 (Potential).
FT 110 (Potential).
FT 111 (Potential).
FT 112 (Potential).
FT 113 (Potential).
FT 114 (Potential).
FT 115 (Potential).
FT 116 (Potential).
FT 117 (Potential).
FT 118 (Potential).
FT 119 (Potential).
FT 120 (Potential).
FT 121 (Potential).
FT 122 (Potential).
FT 123 (Potential).
FT 124 (Potential).
FT 125 (Potential).
FT 126 (Potential).
FT 127 (Potential).
FT 128 (Potential).
FT 129 (Potential).
FT 130 (Potential).
FT 131 (Potential).
FT 132 (Potential).
FT 133 (Potential).
FT 134 (Potential).
FT 135 (Potential).
FT 136 (Potential).
FT 137 (Potential).
FT 138 (Potential).
FT 139 (Potential).
FT 140 (Potential).
FT 141 (Potential).
FT 142 (Potential).
FT 143 (Potential).
FT 144 (Potential).
FT 145 (Potential).
FT 146 (Potential).
FT 147 (Potential).
FT 148 (Potential).
FT 149 (Potential).
FT 150 (Potential).
FT 151 (Potential).
FT 152 (Potential).
FT 153 (Potential).
FT 154 (Potential).
FT 155 (Potential).
FT 156 (Potential).
FT 157 (Potential).
FT 158 (Potential).
FT 159 (Potential).
FT 160 (Potential).
FT 161 (Potential).
FT 162 (Potential).
FT 163 (Potential).
FT 164 (Potential).
FT 165 (Potential).
FT 166 (Potential).
FT 167 (Potential).
FT 168 (Potential).
FT 169 (Potential).
FT 170 (Potential).
FT 171 (Potential).
FT 172 (Potential).
FT 173 (Potential).
FT 174 (Potential).
FT 175 (Potential).
FT 176 (Potential).
FT 177 (Potential).
FT 178 (Potential).
FT 179 (Potential).
FT 180 (Potential).
FT 181 (Potential).
FT 182 (Potential).
FT 183 (Potential).
FT 184 (Potential).
FT 185 (Potential).
FT 186 (Potential).
FT 187 (Potential).
FT 188 (Potential).
FT 189 (Potential).
FT 190 (Potential).
FT 191 (Potential).
FT 192 (Potential).
FT 193 (Potential).
FT 194 (Potential).
FT 195 (Potential).
FT 196 (Potential).
FT 197 (Potential).
FT 198 (Potential).
FT 199 (Potential).
FT 200 (Potential).
FT 201 (Potential).
FT 202 (Potential).
FT 203 (Potential).
FT 204 (Potential).
FT 205 (Potential).
FT 206 (Potential).
FT 207 (Potential).
FT 208 (Potential).
FT 209 (Potential).
FT 210 (Potential).
FT 211 (Potential).
FT 212 (Potential).
FT 213 (Potential).
FT 214 (Potential).
FT 215 (Potential).
FT 216 (Potential).
FT 217 (Potential).
FT 218 (Potential).
FT 219 (Potential).
FT 220 (Potential).
FT 221 (Potential).
FT 222 (Potential).
FT 223 (Potential).
FT 224 (Potential).
FT 225 (Potential).
FT 226 (Potential).
FT 227 (Potential).
FT 228 (Potential).
FT 229 (Potential).
FT 230 (Potential).
FT 231 (Potential).
FT 232 (Potential).
FT 233 (Potential).
FT 234 (Potential).
FT 235 (Potential).
FT 236 (Potential).
FT 237 (Potential).
FT 238 (Potential).
FT 239 (Potential).
FT 240 (Potential).
FT 241 (Potential).
FT 242 (Potential).
FT 243 (Potential).
FT 244 (Potential).
FT 245 (Potential).
FT 246 (Potential).
FT 247 (Potential).
FT 248 (Potential).
FT 249 (Potential).
FT 250 (Potential).
FT 251 (Potential).
FT 252 (Potential).
FT 253 (Potential).
FT 254 (Potential).
FT 255 (Potential).
FT 256 (Potential).
FT 257 (Potential).
FT 258 (Potential).
FT 259 (Potential).
FT 260 (Potential).
FT 261 (Potential).
FT 262 (Potential).
FT 263 (Potential).
FT 264 (Potential).
FT 265 (Potential).
FT 266 (Potential).
FT 267 (Potential).
FT 268 (Potential).
FT 269 (Potential).
FT 270 (Potential).
FT 271 (Potential).
FT 272 (Potential).
FT 273 (Potential).
FT 274 (Potential).
FT 275 (Potential).
FT 276 (Potential).
FT 277 (Potential).
FT 278 (Potential).
FT 279 (Potential).
FT 280 (Potential).
FT 281 (Potential).
FT 282 (Potential).
FT 283 (Potential).
FT 284 (Potential).
FT 285 (Potential).
FT 286 (Potential).
FT 287 (Potential).
FT 288 (Potential).
FT 289 (Potential).
FT 290 (Potential).
FT 291 (Potential).
FT 292 (Potential).
FT 293 (Potential).
FT 294 (Potential).
FT 295 (Potential).
FT 296 (Potential).
FT 297 (Potential).
FT 298 (Potential).
FT 299 (Potential).
FT 300 (Potential).
FT 301 (Potential).
FT 302 (Potential).
FT 303 (Potential).
FT 304 (Potential).
FT 305 (Potential).
FT 306 (Potential).
FT 307 (Potential).
FT 308 (Potential).
FT 309 (Potential).
FT 310 (Potential).
FT 311 (Potential).
FT 312 (Potential).
FT 313 (Potential).
FT 314 (Potential).
FT 315 (Potential).
FT 316 (Potential).
FT 317 (Potential).
FT 318 (Potential).
FT 319 (Potential).
FT 320 (Potential).
FT 321 (Potential).
FT 322 (Potential).
FT 323 (Potential).
FT 324 (Potential).
FT 325 (Potential).
FT 326 (Potential).
FT 327 (Potential).
FT 328 (Potential).
FT 329 (Potential).
FT 330 (Potential).
FT 331 (Potential).
FT 332 (Potential).
FT 333 (Potential).
FT 334 (Potential).
FT 335 (Potential).
FT 336 (Potential).
FT 337 (Potential).
FT 338 (Potential).
FT 339 (Potential).
FT 340 (Potential).
FT 341 (Potential).
FT 342 (Potential).
FT 343 (Potential).
FT 344 (Potential).
FT 345 (Potential).
FT 346 (Potential).
FT 347 (Potential).
FT 348 (Potential).
FT 349 (Potential).
FT 350 (Potential).
FT 351 (Potential).
FT 352 (Potential).
FT 353 (Potential).
FT 354 (Potential).
FT 355 (Potential).
FT 356 (Potential).
FT 357 (Potential).
FT 358 (Potential).
FT 359 (Potential).
FT 360 (Potential).
FT 361 (Potential).
FT 362 (Potential).
FT 363 (Potential).
FT 364 (Potential).
FT 365 (Potential).
FT 366 (Potential).
FT 367 (Potential).
FT 368 (Potential).
FT 369 (Potential).
FT 370 (Potential).
FT 371 (Potential).
FT 372 (Potential).
FT 373 (Potential).
FT 374 (Potential).
FT 375 (Potential).
FT 376 (Potential).
FT 377 (Potential).
FT 378 (Potential).
FT 379 (Potential).
FT 380 (Potential).
FT 381 (Potential).
FT 382 (Potential).
FT 383 (Potential).
FT 384 (Potential).
FT 385 (Potential).
FT 386 (Potential).
FT 387 (Potential).
FT 388 (Potential).
FT 389 (Potential).
FT 390 (Potential).
FT 391 (Potential).
FT 392 (Potential).
FT 393 (Potential).
FT 394 (Potential).
FT 395 (Potential).
FT 396 (Potential).
FT 397 (Potential).
FT 398 (Potential).
FT 399 (Potential).
FT 400 (Potential).
FT 401 (Potential).
FT 402 (Potential).
FT 403 (Potential).
FT 404 (Potential).
FT 405 (Potential).
FT 406 (Potential).
FT 407 (Potential).
FT 408 (Potential).
FT 409 (Potential).
FT 410 (Potential).
FT 411 (Potential).
FT 412 (Potential).
FT 413 (Potential).
FT 414 (Potential).
FT 415 (Potential).
FT 416 (Potential).
FT 417 (Potential).
FT 418 (Potential).
FT 419 (Potential).
FT 420 (Potential).
FT 421 (Potential).
FT 422 (Potential).
FT 423 (Potential).
FT 424 (Potential).
FT 425 (Potential).
FT 426 (Potential).
FT 427 (Potential).
FT 428 (Potential).
FT 429 (Potential).
FT 430 (Potential).
FT 431 (Potential).
FT 432 (Potential).
FT 433 (Potential).
FT 434 (Potential).
FT 435 (Potential).
FT 436 (Potential).
FT 437 (Potential).
FT 438 (Potential).
FT 439 (Potential).
FT 440 (Potential).
FT 441 (Potential).
FT 442 (Potential).
FT 443 (Potential).
FT 444 (Potential).
FT 445 (Potential).
FT 446 (Potential).
FT 447 (Potential).
FT 448 (Potential).
FT 449 (Potential).
FT 450 (Potential).
FT 451 (Potential).
FT 452 (Potential).
FT 453 (Potential).
FT 454 (Potential).
FT 455 (Potential).
FT 456 (Potential).
FT 457 (Potential).
FT 458 (Potential).
FT 459 (Potential).
FT 460 (Potential).
FT 461 (Potential).
FT 462 (Potential).
FT 463 (Potential).
FT 464 (Potential).
FT 465 (Potential).
FT 466 (Potential).
FT 467 (Potential).
FT 468 (Potential).
FT 469 (Potential).
FT 470 (Potential).
FT 471 (Potential).
FT 472 (Potential).
FT 473 (Potential).
FT 474 (Potential).
FT 475 (Potential).
FT 476 (Potential).
FT 477 (Potential).
FT 478 (Potential).
FT 479 (Potential).
FT 480 (Potential).
FT 481 (Potential).
FT 482 (Potential).
FT 483 (Potential).
FT 484 (Potential).
FT 485 (Potential).
FT 486 (Potential).
FT 487 (Potential).
FT 488 (Potential).
FT 489 (Potential).
FT 490 (Potential).
FT 491 (Potential).
FT 492 (Potential).
FT 493 (Potential).
FT 494 (Potential).
FT 495 (Potential).
FT 496 (Potential).
FT 497 (Potential).
FT 498 (Potential).
FT 499 (Potential).
FT 500 (Potential).
FT 501 (Potential).
FT 502 (Potential).
FT 503 (Potential).
FT 504 (Potential).
FT 505 (Potential).
FT 506 (Potential).
FT 507 (Potential).
FT 508 (Potential).
FT 509 (Potential).
FT 510 (Potential).
FT 511 (Potential).
FT 512 (Potential).
FT 513 (Potential).
FT 514 (Potential).
FT 515 (Potential).
FT 516 (Potential).
FT 517 (Potential).
FT 518 (Potential).
FT 519 (Potential).
FT 520 (Potential).
FT 521 (Potential).
FT 522 (Potential).
FT 523 (Potential).
FT 524 (Potential).
FT 525 (Potential).
FT 526 (Potential).
FT 527 (Potential).
FT 528 (Potential).
FT 529 (Potential).
FT 530 (Potential).
FT 531 (Potential).
FT 532 (Potential).
FT 533 (Potential).
FT 534 (Potential).
FT 535 (Potential).
FT 536 (Potential).
FT 537 (Potential).
FT 538 (Potential).
FT 539 (Potential).
FT 540 (Potential).
FT 541 (Potential).
FT 542 (Potential).
FT 543 (Potential).
FT 544 (Potential).
FT 545 (Potential).
FT 546 (Potential).
FT 547 (Potential).
FT 548 (Potential).
FT 549 (Potential).
FT 550 (Potential).
FT 551 (Potential).
FT 552 (Potential).
FT 553 (Potential).
FT 554 (Potential).
FT 555 (Potential).
FT 556 (Potential).
FT 557 (Potential).
FT 558 (Potential).
FT 559 (Potential).
FT 560 (Potential).
FT 561 (Potential).
FT 562 (Potential).
FT 563 (Potential).
FT 564 (Potential).
FT 565 (Potential).
FT 566 (Potential).
FT 567 (Potential).
FT 568 (Potential).
FT 569 (Potential).
FT 570 (Potential).
FT 571 (Potential).
FT 572 (Potential).
FT 573 (Potential).
FT 574 (Potential).
FT 575 (Potential).
FT 576 (Potential).
FT 577 (Potential).
FT 578 (Potential).
FT 579 (Potential).
FT 580 (Potential).
FT 581 (Potential).
FT 582 (Potential).
FT 583 (Potential).
FT 584 (Potential).
FT 585 (Potential).
FT 586 (Potential).
FT 587 (Potential).
FT 588 (Potential).
FT 589 (Potential).
FT 590 (Potential).
FT 591 (Potential).
FT 592 (Potential).
FT 593 (Potential).
FT 594 (Potential).
FT 595 (Potential).
FT 596 (Potential).
FT 597 (Potential).
FT 598 (Potential).
FT 599 (Potential).
FT 600 (Potential).
FT 601 (Potential).
FT 602 (Potential).
FT 603 (Potential).
FT 604 (Potential).
FT 605 (Potential).
FT 606 (Potential).
FT 607 (Potential).
FT 608 (Potential).
FT 609 (Potential).
FT 610 (Potential).
FT 611 (Potential).
FT 612 (Potential).
FT 613 (Potential).
FT 614 (Potential).
FT 615 (Potential).
FT 616 (Potential).
FT 617 (Potential).
FT 618 (Potential).
FT 619 (Potential).
FT 620 (Potential).
FT 621 (Potential).
FT 622 (Potential).
FT 623 (Potential).
FT 624 (Potential).
FT 625 (Potential).
FT 626 (Potential).
FT 627 (Potential).
FT 628 (Potential).
FT 629 (Potential).
FT 630 (Potential).
FT 631 (Potential).
FT 632 (Potential).
FT 633 (Potential).
FT 634 (Potential).
FT 635 (Potential).
FT 636 (Potential).
FT 637 (Potential).
FT 638 (Potential).
FT 639 (Potential).
FT 640 (Potential).
FT 641 (Potential).
FT 642 (Potential).
FT 643 (Potential).
FT 644 (Potential).
FT 645 (Potential).
FT 646 (Potential).
FT 647 (Potential).
FT 648 (Potential).
FT 649 (Potential).
FT 650 (Potential).
FT 651 (Potential).
FT 652 (Potential).
FT 653 (Potential).
FT 654 (Potential).
FT 655 (Potential).
FT 656 (Potential).
FT 657 (Potential).
FT 658 (Potential).
FT 659 (Potential).
FT 660 (Potential).
FT 661 (Potential).
FT 662 (Potential).
FT 663 (Potential).
FT 664 (Potential).
FT 665 (Potential).
FT 666 (Potential).
FT 667 (Potential).
FT 668 (Potential).
FT 669 (Potential).
FT 670 (Potential).
FT 671 (Potential).
FT 672 (Potential).
FT 673 (Potential).
FT 674 (Potential).
FT 675 (Potential).
FT 676 (Potential).
FT 677 (Potential).
FT 678 (Potential).
FT 679 (Potential).
FT 680 (Potential).
FT 681 (Potential).
FT 682 (Potential).
FT 683 (Potential).
FT 684 (Potential).
FT 685 (Potential).
FT 686 (Potential).
FT 687 (Potential).
FT 688 (Potential).
FT 689 (Potential).
FT 690 (Potential).
FT 691 (Potential).
FT 692 (Potential).
FT 693 (Potential).
FT 694 (Potential).
FT 695 (Potential).
FT 696 (Potential).
FT 697 (Potential).
FT 698 (Potential).
FT 699 (Potential).
FT 700 (Potential).
FT 701 (Potential).
FT 702 (Potential).
FT 703 (Potential).
FT 704 (Potential).
FT 705 (Potential).
FT 706 (Potential).
FT 707 (Potential).
FT 708 (Potential).
FT 709 (Potential).
FT 710 (Potential).
FT 711 (Potential).
FT 712 (Potential).
FT 713 (Potential).
FT 714 (Potential).
FT 715 (Potential).
FT 716 (Potential).
FT 717 (Potential).
FT 718 (Potential).
FT 719 (Potential).
FT 720 (Potential).
FT 721 (Potential).
FT 722 (Potential).
FT 723 (Potential).
FT 724 (Potential).
FT 725 (Potential).
FT 726 (Potential).
FT 727 (Potential).
FT 728 (Potential).
FT 729 (Potential).
FT 730 (Potential).
FT 731 (Potential).
FT 732 (Potential).
FT 733 (Potential).
FT 734 (Potential).
FT 735 (Potential).
FT 736 (Potential).
FT 737 (Potential).
FT 738 (Potential).
FT 739 (Potential).
FT 740 (Potential).
FT 741 (Potential).
FT 742 (Potential).
FT 743 (Potential).
FT 744 (Potential).
FT 745 (Potential).
FT 746 (Potential).
FT 747 (Potential).
FT 748 (Potential).
FT 749 (Potential).
FT 750 (Potential).
FT 751 (Potential).
FT 752 (Potential).
FT 753 (Potential).
FT 754 (Potential).
FT 755 (Potential).
FT 756 (Potential).
FT 757 (Potential).
FT 758 (Potential).
FT 759 (Potential).
FT 760 (Potential).
FT 761 (Potential).
FT 762 (Potential).
FT 763 (Potential).
FT 764 (Potential).
FT 765 (Potential).
FT 766 (Potential).
FT 767 (Potential).
FT 768 (Potential).
FT 769 (Potential).
FT 770 (Potential).
FT 771 (Potential).
FT 772 (Potential).
FT 773 (Potential).
FT 774 (Potential).
FT 775 (Potential).
FT 776 (Potential).
FT 777 (Potential).
FT 778 (Potential).
FT 779 (Potential).
FT 780 (Potential).
FT 781 (Potential).
FT 782 (Potential).
FT 783 (Potential).
FT 784 (Potential).
FT 785 (Potential).
FT 786 (Potential).
FT 787 (Potential).
FT 788 (Potential).
FT 789 (Potential).
FT 790 (Potential).
FT 791 (Potential).
FT 792 (Potential).
FT 793 (Potential).
FT 794 (Potential).
FT 795 (Potential).
FT 796 (Potential).
FT 797 (Potential).
FT 798 (Potential).
FT 799 (Potential).
FT 800 (Potential).
FT 801 (Potential).
FT 802 (Potential).
FT 803 (Potential).
FT 804 (Potential).
FT 805 (Potential).
FT 806 (Potential).
FT 807 (Potential).
FT 808 (Potential).
FT 809 (Potential).
FT 810 (Potential).
FT 811 (Potential).
FT 812 (Potential).
FT 813 (Potential).
FT 814 (Potential).
FT 815 (Potential).
FT 816 (Potential).
FT 817 (Potential).
FT 818 (Potential).
FT 819 (Potential).
FT 820 (Potential).
FT 821 (Potential).
FT 822 (Potential).
FT 823 (Potential).
FT 824 (Potential).
FT 825 (Potential).
FT 826 (Potential).
FT 827 (Potential).
FT 828 (Potential).
FT 829 (Potential).
FT 830 (Potential).
FT 831 (Potential).
FT 832 (Potential).
FT 833 (Potential).
FT 834 (Potential).
FT 835 (Potential).
FT 836 (Potential).
FT 837 (Potential).
FT 838 (Potential).
FT 839 (Potential).
FT 840 (Potential).
FT 841 (Potential).
FT 842 (Potential).
FT 843 (Potential).
FT 844 (Potential).
FT 845 (Potential).
FT 846 (Potential).
FT 847 (Potential).
FT 848 (Potential).
FT 849 (Potential).
FT 850 (Potential).
FT 851 (Potential).
FT 852 (Potential).
FT 853 (Potential).
FT 854 (Potential).
FT 855 (Potential).
FT 856 (Potential).
FT 857 (Potential).
FT 858 (Potential).
FT 859 (Potential).
FT 860 (Potential).
FT 861 (Potential).
FT 862 (Potential).
FT 863 (Potential).
FT 864 (Potential).
FT 865 (Potential).
FT 866 (Potential).
FT 867 (Potential).
FT 868 (Potential).
FT 869 (Potential).
FT 870 (Potential).
FT 871 (Potential).
FT 872 (Potential).
FT 873 (Potential).
FT 874 (Potential).
FT 875 (Potential).
FT 876 (Potential).
FT 877 (Potential).
FT 878 (Potential).
FT 879 (Potential).
FT 880 (Potential).
FT 881 (Potential).
FT 882 (Potential).
FT 883 (Potential).
FT 884 (Potential).
FT 885 (Potential).
FT 886 (Potential).
FT 887 (Potential).
FT 888 (Potential).
FT 889 (Potential).
FT 890 (Potential).
FT 891 (Potential).
FT 892 (Potential).
FT 893 (Potential).
FT 894 (Potential).
FT 895 (Potential).
FT 896 (Potential).
FT 897 (Potential).
FT 898 (Potential).
FT 899 (Potential).
FT 900 (Potential).
FT 901 (Potential).
FT 902 (Potential).
FT 903 (Potential).
FT 904 (Potential).
FT 905 (Potential).
FT 906 (Potential).
FT 907 (Potential).
FT 908 (Potential).
FT 909 (Potential).
FT 910 (Potential).
FT 911 (Potential).
FT 912 (Potential).
FT 913 (Potential).
FT 914 (Potential).
FT 915 (Potential).
FT 916 (Potential).
FT 917 (Potential).
FT 918 (Potential).
FT 919 (Potential).
FT 920 (Potential).
FT 921 (Potential).
FT 922 (Potential).
FT 923 (Potential).
FT 924 (Potential).
FT 925 (Potential).
FT 926 (Potential).
FT 927 (Potential).
FT 928 (Potential).
FT 929 (Potential).
FT 930 (Potential).
FT 931 (Potential).
FT 932 (Potential).
FT 933 (Potential).
FT 934 (Potential).
FT 935 (Potential).
FT 936 (Potential).
FT 937 (Potential).
FT 938 (Potential).
FT 939 (Potential).
FT 940 (Potential).
FT 941 (Potential).
FT 942 (Potential).
FT 943 (Potential).
FT 944 (Potential).
FT 945 (Potential).
FT 946 (Potential).
FT 947 (Potential).
FT 948 (Potential).
FT 949 (Potential).
FT 950 (Potential).
FT 951 (Potential).
FT 952 (Potential).
FT 953 (Potential).
FT 954 (Potential).
FT 955 (Potential).
FT 956 (Potential).
FT 957 (Potential).
FT 958 (Potential).
FT 959 (Potential).
FT 960 (Potential).
FT 961 (Potential).
FT 962 (Potential).
FT 963 (Potential).
FT 964 (Potential).
FT 965 (Potential).
FT 966 (Potential).
FT 967 (Potential).
FT 968 (Potential).
FT 969 (Potential).
FT 970 (Potential).
FT 971 (Potential).
FT 972 (Potential).
FT 973 (Potential).
FT 974 (Potential).
FT 975 (Potential).
FT 976 (Potential).
FT 977 (Potential).
FT 978 (Potential).
FT 979 (Potential).
FT 980 (Potential).
FT 981 (Potential).
FT 982 (Potential).
FT 983 (Potential).
FT 984 (Potential).
FT 985 (Potential).
FT 986 (Potential).
FT 987 (Potential).
FT 988 (Potential).
FT 989 (Potential).
FT 990 (Potential).
FT 991 (Potential).
FT 992 (Potential).
FT 993 (Potential).
FT 994 (Potential).
FT 995 (Potential).
FT 996 (Potential).
FT 997 (Potential).
FT 998 (Potential).
FT 999 (Potential).
FT 1000 (Potential).

```

```

QY 146 EGIYLHSLIFMAFFSEKKYLWGFTTFGWLPAVFAVAVWGVRAVLANTGCDLSSGHKKW 205
DB 302 EGIYLHSLIFMAFFSEKKYLWGFTTFGWLPAVFAVAVWGVRAVLANTGCDLSSGHKKW 361
QY 206 IIQVPILASVNLFILFINIIRVATKLRETNAGRCDTQQYRKLLRSTLVLPFGVHY 265
DB 362 IIQVPILASVNLFILFINIIRVATKLRETNAGRCDTQQYRKLLRSTLVLPFGVHY 421
QY 266 TVFMALPYTEVSGTLWQIOHMYEMLFNSFGQFFVAILIYFCNGEVOAEIRKSWRTAL 325
DB 422 TVFMALPYTEVSGTLWQIOHMYEMLFNSFGQFFVAILIYFCNGEVOAEIRKSWRTAL 481
QY 326 DFKRKARSGSSSYSGPM 343
DB 482 DFKRKARSGSSSYSGPM 499

RESULT 5
Q76N28 PRELIMINARY; PRT; 147 AA.
AC Q76N28;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Parathyroid hormone/parathyroid hormone related protein receptor
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=99124508; PubMed=9927318; DOI=10.1210/en.140.2.871;
RA Kawane T., Horiuchi N.;
RT "Insulin-like growth factor I suppresses parathyroid hormone
RT (PTH)/PTH-related protein receptor expression via a mitogen-activated
RT protein kinase pathway in UMR-106 osteoblast-like cells.";
RL Endocrinology 140:871-879 (1999).
DR EMBL; AB012944; BAA36563.1; -.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0004930; F.G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F.parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F.receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00393; PTRHORMONER.
DR PROSITE; PS00650; G_PROTEIN_RECIP_F2_2; 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 147 AA; 15831 MW; 232775272C50B0A1 CRC64;
Query Match 32.4%; Score 141; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 MLFNSFGQFFVAILIYFCNGEVOAEIRKSWRTALDFKARSGSSSYSGPMVSHTS 348
DB 1 MLFNSFGQFFVAILIYFCNGEVOAEIRKSWRTALDFKARSGSSSYSGPMVSHTS 60
QY 349 VTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPGCAPATETTLPTVWAVPKDDGFLNG 408
DB 61 VTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPGCAPATETTLPTVWAVPKDDGFLNG 120
QY 409 SCSGLDEEASGSARPPPLQEQ 429
DB 121 SCSGLDEEASGSARPPPLQEQ 141

RESULT 6
PTRR_HUMAN

```

ID	PTHR_HUMAN	STANDARD;	PRT;	593 AA.
AC	Q03431;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Parathyroid hormone/parathyroid hormone-related peptide receptor			
DE	precursor (PTH/PTHrP receptor) (PTH/PTHrP type I receptor).			
GN	Name=PTHRI; Synonyms=PTHr;			
OS	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=93238641; PubMed=8386612; DOI=10.1210/en.132.5.2157;			
RA	Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,			
RA	Abou-Samra A.-B., Segre G.V., Jueppner H.;			
RT	"Identical complementary deoxyribonucleic acids encode a human renal			
RT	and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";			
RL	Endocrinology 132:2157-2165(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=93387403; PubMed=8397094; DOI=10.1016/0922-4106(93)90092-N;			
RA	Schneider H., Feyen J.-H., Rao Movva N.;			
RT	"Cloning and functional expression of a human parathyroid hormone			
RT	receptor.";			
RL	Eur. J. Pharmacol. 246:149-155(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95263723; PubMed=7745008; DOI=10.1210/jc.80.5.1611;			
RA	Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,			
RA	Stuhrmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,			
RA	Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,			
RA	Abou-Samra A.-B., Segre G.V., Jueppner H.;			
RT	"Pseudohypoparathyroidism type Ib is not caused by mutations in the			
RT	coding exons of the human parathyroid hormone (PTH)/PTH-related			
RT	peptide receptor gene.";			
RL	J. Clin. Endocrinol. Metab. 80:1611-1621(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Levine M.A.;			
RT	"Characterization of cDNA and genomic DNA encoding the human PTH/PTHrP			
RT	receptor.";			
RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	EXTRACELLULAR DOMAIN DISULFIDE BONDS.			
RX	MEDLINE=20374569; PubMed=10913300; DOI=10.1021/bi0001426;			
RA	Grauschopf U., Lilie H., Honold K., Wozny M., Reusch D., Esswein A.,			
RA	Schafer W., Rucknagel K.P., Rudolph R.;			
RT	"The N-terminal fragment of human parathyroid hormone receptor 1			
RT	constitutes a hormone binding domain and reveals a distinct disulfide			
RT	pattern.";			
RL	Biochemistry 39:8878-8887(2000).			
RN	[6]			
RP	STRUCTURE BY NMR OF 169-198.			
RX	MEDLINE=98409426; PubMed=9737850; DOI=10.1021/bi981265h;			
RA	Pellegrini M., Bisello A., Rosenthal M., Chorev M., Mierke D.P.;			
RT	"Binding domain of human parathyroid hormone receptor: from			
RT	conformation to function.";			
RL	Biochemistry 37:12737-12743(1998).			
RN	[7]			
RP	VARIANT JMC ARG-223.			
RX	MEDLINE=95215874; PubMed=7701349;			
RA	Schipani E., Kruse K., Jueppner H.;			
RT	"A constitutively active mutant PTH-PTHrP receptor in Jansen-type			
RT	metaphyseal chondrodysplasia.";			
RL	Science 268:98-100(1995).			
RN	[8]			
RP	VARIANTS JMC ARG-223 AND PRO-410.			
RX	MEDLINE=96366745; PubMed=8703170; DOI=10.1056/NEJM199609053351004;			

RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
RA Kooh S.W., Cole W.G., Jueppner H.;

RT "Constitutively activated receptors for parathyroid hormone and
RT parathyroid hormone-related peptide in Jansen's metaphyseal
RT chondrodysplasia.";

RL N. Engl. J. Med. 335:708-714(1996).

RN [9]

RP CHARACTERIZATION OF VARIANTS JMC ARG-223 AND PRO-410.
RX MEDLINE=97322091; PubMed=9178745; DOI=10.1210/me.11.7.851;

RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
RA Jueppner H.;

RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
RT receptors mutated at the two loci for Jansen's metaphyseal
RT chondrodysplasia.";

RL Mol. Endocrinol. 11:851-858(1997).

RN [10]

RP VARIANT BOCD LSU-132.
RX MEDLINE=98417978; PubMed=9745456; DOI=10.1210/jc.83.9.3373;

RA Zhang P., Robert A.-S., Couvineau A., Silve C.;

RT "A homozygous inactivating mutation in the parathyroid
RT hormone/parathyroid hormone-related peptide receptor causing
RT Blomstrand chondrodysplasia.";

RL J. Clin. Endocrinol. Metab. 83:3365-3368(1998).

RN [11]

RP VARIANT JMC ARG-458.
RX MEDLINE=99415605; PubMed=10487664; DOI=10.1210/jc.84.9.3052;

RA Schipani E., Langman C.B., Hunzelman J., Le Merrier M., Loke K.Y.,
RA Dillon M.J., Silve C., Jueppner H.;

RT "A novel parathyroid hormone (PTH)/PTH-related peptide receptor
RT mutation in Jansen's metaphyseal chondrodysplasia.";

RL J. Clin. Endocrinol. Metab. 84:3052-3057(1999).

RN [12]

RP VARIANT ENCHONDROMATOSIS CVS-150.
RX MEDLINE=21918585; PubMed=11850620; DOI=10.1038/ng844;

RA Hopyan S., Gokgoz N., Poon R., Gensure R.C., Yu C., Cole W.G.,
RA Bell R.S., Jueppner H., Andrulis I.L., Wunder J.S., Alman B.A.;

RT "A mutant PTH/PTHrP type I receptor in enchondromatosis.";

RL Nat. Genet. 30:306-310(2002).

CC -I- FUNCTION: This is a receptor for parathyroid hormone and for
CC parathyroid hormone-related peptide. The activity of this receptor
CC is mediated by G proteins which activate adenylyl cyclase and also
CC a phosphatidylinositol-calcium second messenger system.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein.

CC -I- TISSUE SPECIFICITY: Expressed in most tissues. Most abundant in
CC kidney, bone and liver.

CC -I- DISEASE: Defects in PTHRI are the cause of Jansen's metaphyseal
CC chondrodysplasia (JMC) [MIM:158400]. JMC is a rare autosomal
CC dominant disorder characterized by a short-limbed dwarfism
CC associated with hypercalcemia and normal or low serum
CC concentrations of the two parathyroid hormones.

CC -I- DISEASE: Defects in PTHRI are the cause of chondrodysplasia
CC Blomstrand type (BOCD) [MIM:215045]. BOCD is a severe skeletal
CC dysplasia.

CC -I- DISEASE: Defects in PTHRI can be a cause of enchondromatosis
CC [MIM:166000]. Enchondromas are common benign cartilage tumors of
CC bone. They can occur as solitary lesions or as multiple lesions in
CC enchondromatosis (Ollier and Maffucci diseases). Clinical problems
CC caused by enchondromas include skeletal deformity and the
CC potential for malignant change to osteosarcoma.

CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; L04308; AAA36525.1; -;
CC EMBL; X68596; CAA48589.1; -;
CC EMBL; U22409; AAB60657.1; -;

```

DR EMBL; U22401; AAB60657.1; JOINED.
DR EMBL; U22402; AAB60657.1; JOINED.
DR EMBL; U22403; AAB60657.1; JOINED.
DR EMBL; U22404; AAB60657.1; JOINED.
DR EMBL; U22405; AAB60657.1; JOINED.
DR EMBL; U22406; AAB60657.1; JOINED.
DR EMBL; U22407; AAB60657.1; JOINED.
DR EMBL; U22408; AAB60657.1; JOINED.
DR EMBL; U17418; AAB56774.1; -.
DR PIR; I38139; A49191.
DR PDB; 1BLJ; NMR; @=168-198.
DR PDB; 1ET2; Model; S=168-469.
DR PDB; 1ET3; Model; S=168-469.
DR Genew; HGNC:9608; PTHR1.
DR MIM; 168468; -.
DR MIM; 156400; -.
DR MIM; 215045; -.
DR MIM; 166000; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR 3D-structure; Disease mutation; Dwarfism; G-protein coupled receptor;
KW Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 593
FT DOMAIN 27 188 Parathyroid hormone/parathyroid hormone-
FT TRANSMEM 189 212 related peptide receptor.
FT DOMAIN 213 219 Extracellular (Potential).
FT TRANSMEM 220 239 1 (Potential).
FT DOMAIN 240 282 2 (Potential).
FT TRANSMEM 283 306 Extracellular (Potential).
FT DOMAIN 307 320 3 (Potential).
FT TRANSMEM 321 342 Cytoplasmic (Potential).
FT DOMAIN 343 361 Extracellular (Potential).
FT TRANSMEM 362 382 4 (Potential).
FT DOMAIN 383 409 5 (Potential).
FT TRANSMEM 410 428 Cytoplasmic (Potential).
FT DOMAIN 429 440 6 (Potential).
FT TRANSMEM 441 463 Extracellular (Potential).
FT DOMAIN 464 593 7 (Potential).
FT TRANSMEM 464 593 Cytoplasmic (Potential).

Query Match 11.3%; Score 49; DB 1; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GYACRCVAVTFYFLATNYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
DB 277 GYACRCVAVTFYFLATNYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 7
Q9TU31 PRELIMINARY; PRT; 595 AA.
AC Q9TU31
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor-1.
GN Name=PTH1;

Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167095; AAD55938.1; -.
DR HSSP; Q03431; 1BL1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR Receptor.
SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match 11.3%; Score 49; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GYACRCVAVTFYFLATNYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
DB 276 GYACRCVAVTFYFLATNYWILVEGLYHLSLIFMAFFSEKKYLWGFT 324

RESULT 8
PTHR_PIG STANDARD; PRT; 585 AA.
ID PTHR_PIG
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE Precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).
GN Name=PTHr1; Synonyms=PTHr;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305358; PubMed=8688470; DOI=10.1016/0167-4781(96)00035-8;
RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
RA Chandrasekhar S., Hsiung H.M.;
RT "Structure and functional expression of a complementary DNA for
RT porcine parathyroid hormone/parathyroid hormone-related peptide
RT receptor.";
RL Blochim. Biophys. Acta 1307:339-347(1996).
CC -!- FUNCTION: This is a receptor for parathyroid hormone and for
CC parathyroid hormone-related peptide. The activity of this receptor
CC is mediated by G proteins which activate adenylyl cyclase and also
CC a phosphatidylinositol-calcium second messenger system (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```


use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; U18315; AAC48619.1; -;
HSP; Q03431; IBL1.
DR InterPro; IPR000832; GPCR secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HORMR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 585
FT DOMAIN 27 184 Parathyroid hormone/parathyroid hormone-related peptide receptor.
FT DOMAIN 185 208 Extracellular (Potential).
FT DOMAIN 209 215 1 (Potential).
FT TRANSMEM 216 235 Cytoplasmic (Potential).
FT DOMAIN 236 277 2 (Potential).
FT TRANSMEM 278 301 Extracellular (Potential).
FT DOMAIN 302 315 3 (Potential).
FT TRANSMEM 316 337 Cytoplasmic (Potential).
FT DOMAIN 338 356 4 (Potential).
FT TRANSMEM 357 377 Extracellular (Potential).
FT DOMAIN 378 404 5 (Potential).
FT TRANSMEM 405 423 Cytoplasmic (Potential).
FT DOMAIN 424 435 Extracellular (Potential).
FT TRANSMEM 436 458 Extracellular (Potential).
FT DOMAIN 459 585 7 (Potential).
FT DISULFID 48 113 By similarity.
FT DISULFID 104 144 By similarity.
FT DISULFID 127 166 By similarity.
FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 162 162 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;
Query Match 10.6%; Score 46; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 124 GCRVATFFLYFLATNYWILVEGLYHSLIFMAFFSEKKYLWGFT 169
Db 275 GCRVATFFLYFLATNYWILVEGLYHSLIFMAFFSEKKYLWGFT 320
RESULT 9
Q9GMD1
ID Q9GMD1 PRELIMINARY; PRT; 589 AA.
AC Q9GMD1.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PTH/PTHR type I receptor.
GN Name=PTHR;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP TISSUE=Kidney.
RA McLaughern-Carucci J.F., Mitnick M., Emanuel J.R., Dworetzky S.I.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288463; AAG09046.1; -;

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Pthrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR SMART; SM00008; HORMR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 589 AA; 64017 MW; 5PFD5DF8861E72BB CRC64;
Query Match 9.9%; Score 43; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 272 PYTEVSGTLAQIQHVEMLFNSFGGFVVAIYFCNGEVOAEI 314
Db 427 PYTEVSGTLAQIQHVEMLFNSFGGFVVAIYFCNGEVOAEI 469
RESULT 10
Q8NHB4
ID Q8NHB4 PRELIMINARY; PRT; 964 AA.
AC Q8NHB4.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsuni S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB065462; BAC05721.1; -;
DR HSP; Q03431; IBL1.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Pthrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00393; PTRHORMONER.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 964 AA; 105705 MW; 8EA72B44244DFD5D CRC64;
Query Match 9.9%; Score 43; DB 2; Length 964;
Best Local Similarity 100.0%; Pred. No. 2e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 127 VAVTFYFLATNYWILVEGLYHSLIFMAFFSEKKYLWGFT 169
Db 557 VAVTFYFLATNYWILVEGLYHSLIFMAFFSEKKYLWGFT 599
RESULT 11
Q7YR13

"Zebrafish express the common parathyroid hormone/parathyroid hormone-related peptide receptor (PTH1R) and a novel receptor (PTH3R) that is preferentially activated by mammalian and fugu fish parathyroid hormone-related peptide.";
J. Biol. Chem. 274:28185-28190(1999).

DR EMBL: AF132084; AAF01265.1; --
DR HSSP: Q03431; 1BL1.
DR ZFIN: ZDB-GENE-991123-8; pthrl.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO: GO:0004991; F:parathyroid hormone receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR001879; Hormn_receptor.
DR InterPro: IPR002170; Phrmn_receptor.
DR Pfam: PF00002; 7tm 2; 1.
DR Pfam: PF02793; HRM; 1.
DR PRINTS: PR00249; GPCRSECRETIN.
DR PRINTS: PR00393; PTHORMONER.
DR SMART: SM00008; Hormr; 1.
DR PROSITE: PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE: PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE: PS02027; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE: PS02026; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.

SO SEQUENCE 536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;

Query Match 6.4%; Score 28; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 4.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 NIIRVATKLRETNAGRCDDTQVYRKL 251

Db 334 NIIRVATKLRETNAGRCDDTQVYRKL 361

RESULT 14

O9PRG1 PRELIMINARY; PRT; 94 AA.
AC O9PRG1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Parathyroid hormone type-2 receptor (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99367425; PubMed=10438471; DOI=10.1074/jbc.274.33.23035;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human parathyroid hormone and not by human or teleost parathyroid hormone-related peptide. Implications for the evolutionary conservation of calcium-regulating peptide hormones";
RL J. Biol. Chem. 274:23035-23042(1999).
DR EMBL: AF132081; AAD51907.1; --
DR EMBL: AF132078; AAD51906.1; --
DR EMBL: AF132079; AAD51906.1; JOINED.
DR EMBL: AF132080; AAD51906.1; JOINED.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR000832; GPCR_secretin.
DR Pfam: PF00002; 7tm 2; 1.
DR PRINTS: PR00249; GPCRSECRETIN.
DR PROSITE: PS02026; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
FT NON_TER 94 94

SO SEQUENCE 94 AA; 10729 MW; D949182E1D2613EF CRC64;

Query Match 6.2%; Score 27; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 YFLATNYWILVEGLYHSLIFMAFPPS 160

Db 12 YFLATNYWILVEGLYHSLIFMAFPPS 38

RESULT 15

O57671 PRELIMINARY; PRT; 126 AA.
AC O57671;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Parathyroid hormone receptor (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsu C., You S., El Halawani M.E., Foster D.N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U94326; AAB93893.1; --
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR000832; GPCR_secretin.
DR Pfam: PF00002; 7tm 2; 1.
DR PRINTS: PR00249; GPCRSECRETIN.
DR PROSITE: PS02026; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
FT NON_TER 126 126

SO SEQUENCE 126 AA; 14515 MW; 0F381BDB094A1A77 CRC64;

Query Match 6.0%; Score 26; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 LVEGLYHSLIFMAFFSEKKYLGFT 169

Db 6 LVEGLYHSLIFMAFFSEKKYLGFT 31

Search completed: July 4, 2005, 06:30:44
Job time : 96 secs

This Page Blank (uspto)